

FIGURE 1

CCAATCGCCCGGTGCGGTGGTGCAGGGTCTCGGGCTAGTCATGGCGTCCCCGTCTCGGAGAC
TGCAGACTAAACCAGTCATTACTTGTTTCAAGAGCGTTCTGCTAATCTACACTTTTATTTTC
TGGATCACTGGCGTTATCCTTCTTGCACTTGGCATTGTTGGGGCAAGGTGAGCCTGGAGAATTA
CTTTTCTCTTTTAAATGAGAAGGCCACCAATGTCCCCTTCGTGCTCATTGCTACTGGTACCG
TCATTATTCTTTTGGGCACCTTTGGTTGTTTTGCTACCTGCCGAGCTTCTGCATGGATGCTA
AAACTGTATGCAATGTTTCTGACTCTCGTTTTTTTGGTCGAACTGGTCGCTGCCATCGTAGG
ATTTGTTTTTCAGACATGAGATTAAGAACAGCTTTAAGAATAATTATGAGAAGGCTTTGAAGC
AGTATAACTCTACAGGAGATTATAGAAGCCATGCAGTAGACAAGATCCAAAATACGTTGCAT
TGTTGTGGTGTCAACCGATTATAGAGATTGGACAGATACTAATTATTACTCAGAAAAAGGATT
TCCTAAGAGTTGCTGTAAACTTGAAGATTGTACTCCACAGAGAGATGCAGACAAAGTAAACA
ATGAAGGTTGTTTTATAAAGGTGATGACCATTATAGAGTCAGAAATGGGAGTCGTTGCAGGA
ATTTCTTTTGGAGTTGCTTGCTTCCAACCTGATTGGAATCTTTCTCGCCTACTGCCWCTCTCG
TGCCATAACAAATAACCAGTATGAGATAGTGTAACCCAATGTATCTGTGGGCCTATTCCTCT
CTACCTTTAAGGACATTTAGGGTCCCCCTGTGAATTAGAAAGTTGCTTGGCTGGAGAACTG
ACAACACTACTTACTGATAGACCAAAAAACTACACCAGTAGGTTGATTCAATCAAGATGTAT
GTAGACCTAAAACTACACCAATAGGCTGATTCAATCAAGATCCGTGCTCGCAGTGGGCTGAT
TCAATCAAGATGTATGTTTGCTATGTTCTAAGTCCACCTTCTATCCCATTCATGTTAGATCG
TTGAAACCCTGTATCCCTCTGAAACACTGGAAGAGCTAGTAAATTGTAAATGAAGT

FIGURE 2

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA19902
><subunit 1 of 1, 245 aa, 1 stop, 1 unknown
><MW: -1, pI: 8.36, NX(S/T): 1
MASPSRRLQTKPVITCFKSVLLIYTFIFWITGVILLAVGIWGKVSLENYFSLLNEKATNVPF
VLIATGTVIILLGTFGCFATCRASAWMLKLYAMFLTLVFLVELVAAIVGFVFRHEIKNSFKN
NYEKALKQYNSTGDYRSHAVDKIQNTLHCCGVTDYRDWTDNYYSEKGFPSCKLEDCTPQ
RDADKVNNEGCFIKVMTIIESEMGVVAGISFGVACFQLIGIFLAYCXSRITNNQYEIV
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Important features of the protein:**Signal peptide:**

amino acids 1-42

Transmembrane domains:

amino acids 19-42, 61-83, 92-114, 209-230,

N-glycosylation site.

amino acids 134-138

Tyrosine kinase phosphorylation site.

amino acids 160-168, 160-169

N-myristoylation site.

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 69-80, 211-222

FIGURE 3

CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAA
GGAGTCGCGCCGCCGCCGCCGCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGTCAGT
GCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGT
TGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGGG
GCCGGGGTAGGCTCTGGAAAGGGCCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA
GCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCCCTAGAAGAGGGT
GTTCCCTCTTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCCCTTCTGAGGAGGCT
GCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCGTAGATTGATAATGTTG
GGAATAAGCTCTGCAACTTTCTTTGGCATTTCAGTTGTTAAAAACAAATAGGATGCAAAATTC
TCAACTCCAGGTTATGAAAACAGTACTTGAAAACTGAAAACTACCTAAATGATCGTCTTTG
GTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAG
CACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTG
CCGAGATGACAGTGGAACAGATGACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAGTG
CAGTACCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTTCGGCCACCAAGGAGGGGC
CGAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACT
GGCAGTAATACGGACTCTTGTAGATAAGTAAAGTATCTGACTCACGGTCACCTCCAGTGGAAT
GAAAAGTGTTCTGCCCGGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATACTCG
CCAAGCCTTGTGCTCACAGGGCAAAGGAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAA
TGATAAGATTTGATGTTTTTGCTTGCTGTCTACTTTGTCTGGAAATGTCTAAATGTTTC
TGTAGCAGAAAACACGATAAAGCTATGATCTTTATTAGAG

FIGURE 4

MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ
AENSAVPTADTRSQPRDPVRP PRRGRGPHEPRRKKQNV DGLVLDTLAVIRTLVDKO

Signal peptide:

amino acids 1-16

Casein kinase II phosphorylation site.

amino acids 22-26, 50-54, 113-117

N-myristoylation site.

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

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FIGURE 5

GGCACGAGGCGCTGTCCACCCGGGGGCGTGGGAGTGAGGTACCAGATTCAGCCCATTGTTGGCC
CCGACGCCTCTGTTCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCGGTTCCCTAACGGACTG
CAAG**ATG**GAGGAAGGCGGGAACCTAGGAGGCCTGATTAAGATGGTCCATCTACTGGTCTTGT
CAGGTGCCCTGGGGCATGCAAATGTGGGTGACCTTCGTCTCAGGCTTCCTGCTTTTCCGAAGC
CTTCCCCGACATACCTTCGGACTAGTGACAGCAAACCTCTTCCCCTTCTACTTCCACATCTC
CATGGGCTGTGCCCTTCATCAACCTCTGCATCTTGGCTTCACAGCATGCTTGGGCTCAGCTCA
CATTCTGGGAGGCCAGCCAGCTTTACCTGCTGTTCCCTGAGCCTTACGCTGGCCACTGTCAAC
GCCCCTGGCTGGAACCCCGCACACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGA
GCGAGGCCTGGGTGGGGAGGTACCAGGCAGCCACCAGGGTCCCGATCCCTACCGCCAGCTGC
GAGAGAAGGACCCCAAGTACAGTGCTCTCCGCCAGAATTTCTTCCGCTACCATGGGCTGTCC
TCTCTTTGCAATCTGGGCTGCGTCCCTGAGCAATGGGCTCTGTCTCGCTGGCCTTGCCCTGGA
AATAAGGAGCCTC**TAG**CATGGGCCCTGCATGCTAATAAATGCTTCTTCAGAAATGAAAAAA
AAAAAAAAAAAA

FIGURE 6

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56107

<subunit 1 of 1, 231 aa, 1 stop

<NX(S/T): 0

MEEGGLGGLIKMVHLLVLSGAWGMQMWVTFVSGFLLFRSLPRHTFGLVQSKLFPFYFHISM
GCAFINLCILASQHAWAQLTFWEASQLYLLFSLTLATVNARWLEPRTTAAAMWALQTVEKER
GLGGEVPGSHQGPDPYRQLREKDPKYSALRQNFYHGLSSLCNLGCVLSNGLCLAGLALEIRSL

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 86-103, 60-75

Casein kinase II phosphorylation site.

amino acids 82-86

Tyrosine kinase phosphorylation site.

amino acids 144-151

N-myristoylation site.

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 54-65

G-protein coupled receptors proteins.

amino acids 44-85

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FIGURE 7

AATTCAGATTTTAAGCCCATTTCTGCAGTGAATTTTCATGAACTAGCAAGAGGACACCATCTT
CTTGTATTATACAAGAAAGGAGTGTACCTATCACACACAGGGGGGAAAA**ATG**CTCTTTTGGGT
GCTAGGCCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAAACTAAAGATTGAAG
ACATCACTGATAAGTACATTTTTTATCACTGGATGTGACTCGGGCTTTGGAACTTGGCAGCC
AGAACTTTTGATAAAAAGGGATTTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAAC
AGCTTTAAAGGCAGAAACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAG
AGAATGTCAAGAGGACTGCCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGGT
CTGATCAATAATGCTGGTGTTCCTGGCGTGTGGCTCCCACTGACTGGCTGACACTAGAGGA
CTACAGAGAACCTATTGAAGTGAACCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTC
CTTTGGTCAAGAAAGCTCAAGGGAGAGTTATTAATGTCTCCAGTGTGGAGGTCGCCTTGCA
ATCGTTGGAGGGGGCTATACTCCATCCAAATATGCAGTGAAGGTTTCAATGACAGCTTAAG
ACGGGACATGAAAGCTTTTGGTGTGCACGTCTCATGCATTGAACCAGGATTGTTCAAAACAA
ACTTGGCAGATCCAGTAAAGGTAATTGAAAAAACTCGCCATTTGGGAGCAGCTGTCTCCA
GACATCAAACAACAATATGGAGAAGGTTACATTGAAAAAAGTCTAGACAACTGAAAGGCAA
TAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTGCATGGACCACGCTCTAACAA
GTCTCTTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAAATTTTCTGGATACCTCTG
TCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAAGCAGAGCTGGCTAA
TCCCAAGGCAGT**GTGA**CTCAGCTAACCACAAATGTCTCCTCCAGGCTATGAAATTGGCCGAT
TTCAAGAACACATCTCCTTTTCAACCCCATTCCTTATCTGCTCCAACCTGGACTCATTTAGA
TCGTGCTTATTTGGATTGCAAAAGGGAGTCCCACCATCGCTGGTGGTATCCCAGGGTCCCTG
CTCAAGTTTTCTTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCCTGCCCTGT
ATTTAGGCTTTGCCTGCTTGGTGTGATGTAAGGGAAATTGAAAGACTTGCCCATTCAAAATG
ATCTTTACCGTGGCCTGCCCCATGCTTATGGTCCCCAGCATTTACAGTAACTTGTGAATGTT
AAGTATCATCTCTTATCTAAATATTAAAAGATAAGTCAACCCAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAA

FIGURE 8

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56406
><subunit 1 of 1, 319 aa, 1 stop
><MW: 35227, pI: 8.97, NX(S/T): 3
MLFWVLGLLILCGFLWTRKGLKIEDITDKYIFITGCDSGFGNLAARTFDKKGFHVIAACLT
ESGSTALKAETSERLRTVLLDVTDPENVKRTAQWVKNQVGEKGLWGLINNAGVPGVLAPTDW
LTLEDYREPIEVNLFGLISVTLNMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGF
NDSLRRDMKAFGVHVSCIEPGLFKTNLADPVKVIEKKLAIWEQLSPDIKQQYGEGYIEKSLD
KLKGNKSYVNMDLSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQK
AELANPKAV

Important features of the protein:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 136-152

N-glycosylation sites.

amino acids 161-163, 187-190 and 253-256

Glycosaminoglycan attachment site.

amino acids 39-42

N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

FIGURE 9

GCGGGCTGTTGACGGCGCTGCG**ATG**GCTGCCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTT
 CCTCTCAGTCGGA~~CT~~TCTGACGCCGCCAGTGGGCGGGGCCCTTGGGCGGTCGCCACCACT
 GTAGTCATGTACCCACCGCCGCCGCCGCCCTCATCGGGACTTCATCTCGGTGACGCTGAG
 CTTTGGCGAGAGCTATGACAACAGCAAGAGTTGGCGGCGGCGCTCGTGCTGGAGGAAATGGA
 AGCAACTGTCGAGATTGCAGCGGAATATGATTCTCTTCCTCCTTGCCTTTCTGCTTTTCTGT
 GGACTCCTCTTCTACATCAACTTGGCTGACCATTGGAAAGCTCTGGCTTTCAGGCTAGAGGA
 AGAGCAGAAGATGAGGCCAGAAATTGCTGGGTAAAACCAGCAAATCCACCCGTCTTACCAG
 CTCCTCAGAAGGCGGACACCGACCCTGAGAACTTACCTGAGATTTTCGTACAGAAGACACAA
 AGACACATCCAGCGGGGACCACCTCACCTGCAGATTAGACCCCAAGCCAAGACCTGAAGGA
 TGGGACCCAGGAGGAGGCCACAAAAGGCAAGAAGCCCCTGTGGATCCCCGCCGGAAGGAG
 ATCCGCAGAGGACAGTCATCAGCTGGAGGGGAGCGGTGATCGAGCCTGAGCAGGGCACCGAG
 CTCCTTCAAGAAGAGCAGAAGTGCCACCAAGCCTCCCCTGCCACCGGCCAGGACACAGGG
 CACACCAGTGCATCTGAACTATCGCCAGAAGGGCGTGATTGACGTCTTCCTGCATGCATGGA
 AAGGATACCGCAAGTTTGCATGGGGCCATGACGAGCTGAAGCCTGTGTCCAGGTCCCTTCACT
 GAGTGGTTTGGCCTCGGTCTCACACTGATCGACGCGCTGGACACCATGTGGATCTTGGGTCT
 GAGGAAAGAATTTGAGGAAGCCAGGAAGTGGGTGTGAAGAAGTTACACTTTGAAAAGGACG
 TGGACGTCAACCTGTTTGAAGACACGATCCGCATCCTGGGGGGGCTCCTGAGTGCCTACCAC
 CTGTCTGGGGACAGCCTCTTCCTGAGGAAAGCTGAGGATTTTGGAAATCGGCTAATGCCTGC
 CTTCAGAACACCATCCAAGATTCTTACTCGGATGTGAACATCGGTACTGGAGTTGCCACCC
 CGCCACGGTGGACCTCCGACAGCACTGTGGCCGAGGTGACCAGCATTACAGCTGGAGTTCCGG
 GAGCTCTCCCGTCTCACAGGGGATAAGAAGTTTCAGGAGGCAGTGGAGAAGGTGACACAGCA
 CATCCACGGCCTGTCTGGGAAGAAGGATGGGCTGGTGCCCATGTTTCATCAATACCCACAGTG
 GCCTCTTACCCACCTGGGCGTATTCACGCTGGGCGCCAGGGCCGACAGCTACTATGAGTAC
 CTGCTGAAGCAGTGGATCCAGGGCGGGAAGCAGGAGACACAGCTGCTGGAAGACTACGTGGA
 AGCCATCGAGGGTGTGAGAACGCACCTGCTGCGGCACTCCGAGCCCAGTAAGCTCACCTTTG
 TGGGGGAGCTTGCCACGGCCGCTTCACTGCCAAGATGGACCACCTGGTGTGCTTCCTGCCA
 GGGACGCTGGCTCTGGGCGTCTACCACGGCCTGCCCGCCAGCCACATGGAGCTGGCCCAGGA
 GCTCATGGAGACTTGTTACCAGATGAACCGGCAGATGGAGACGGGGCTGAGTCCCGAGATCG
 TGCACTTCAACCTTTACCCCCAGCCGGGCGCTCGGGACGTGGAGGTCAAGCCAGCAGACAGG
 CACAACCTGCTGCGGCCAGAGACCGTGGAGAGCCTGTTCTACCTGTACCGCGTCACAGGGGA
 CCGCAAATACCAGGACTGGGGCTGGGAGATTCTGCAGAGCTTCAGCCGATTCACACGGGTCC
 CCTCGGGTGGCTATTCTTCCATCAACAATGTCCAGGATCCTCAGAAGCCCGAGCCTAGGGAC
 AAGATGGAGAGCTTCTTCCTGGGGGAGACGCTCAAGTATCTGTTCTTGCTCTTCTCCGATGA
 CCCAAACCTGCTCAGCCTGGACGCTACGTGTTCAACACCGAAGCCCACCCTCTGCCTATCT
 GGACCCCTGCC**TAG**GGTGGATGGCTGCTGGTGTGGGGACTTCGGGTGGGCAGAGGCACCTTG
 CTGGGTCTGTGGCATTTTCCAAGGGCCACGTAGCACCGCAACCGCCAAGTGGCCCAGGCT
 CTGAACTGGCTCTGGGCTCCTCCTCGTCTCTGCTTTAATCAGGACACCGTGAGGACAAGTGA
 GGCCGTCACTCTTGGTGTGATGCGGGGTGGGCTGGGCCGCTGGAGCCTCCGCCTGCTTCCTC
 CAGAAGACACGAATCATGACTCACGATTGCTGAAGCCTGAGCAGGTCTCTGTGGGCCGACCA
 GAGGGGGGCTTCGAGGTGGTCCCTGGTACTGGGGTGACCGAGTGGACAGCCCAGGGTGCAGC
 TCTGCCCCGGGCTCGTGAAGCCTCAGATGTCCCAATCCAAGGGTCTGGAGGGGCTGCCGTGA
 CTCCAGAGGCCTGAGGCTCCAGGGCTGGCTCTGGTGTTTACAAGCTGGACTCAGGGATCCTC
 CTGGCCGCCCGCAGGGGGCTTGGAGGGCTGGACGGCAAGTCCGTCTAGCTCACGGGGCCCT
 CCAGTGGAAATGGGTCTTTTCGGTGGAGATAAAAGTTGATTTGCTCTAACCGCAA

FIGURE 10

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56529

><subunit 1 of 1, 699 aa, 1 stop

><MW: 79553, pI: 7.83, NX(S/T): 0

MAACEGRRSGALGSSQSDFLTPFVGAPWAVATTVMYPPPPPPPHRDFISVTLSFGESYDN
SKSWRRRSCWRKWKQLSRLQRNMILFLLAFLLFCGLLFYINLADHWKALAFRLEEEQKMRPE
IAGLKPANPPVLPAPQKADTDPENLPEISSQKTQRHIQRGPPHLQIRPPSQDLKDGTQEEAT
KRQEAPVDPRPEGDPQRTVISWRGAVIEPEQGTELPSRRAEVPTKPPLPPARTQGTPVHLNY
RQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSFSEWFGLGLTLIDALDTMWILGLRKEFEEA
RKWVSKKLHFEKDVDVNLFESTITIRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKI
PYSDVNIGTGVAHPPRWTSdstVAEVTSIQLEFRELsRLTGDKKFQEAVEKVTQHIHGLSGK
KDGLVPMFINTHSGLFTHLGVFTLGARADSYEYLLKQWIQGGKQETQLLEDYVEAIEGVRT
HLLRHSEPSKLTfVgELAHGRFSakMDHLVCFLPGTLALGVYHGLPASHMELAQELMETCYQ
MNRQMETGLSPEIVHFNLYPQPGRRDVEVKPADRHNLRLPETVESLFYLYRVTGDRKYQDWG
WEILQSFSRfTRVPSGGYSSINNVQDPQKPEPRDKMESFFLGETLKYLFLLFSDDPNLLSLD
AYVENTEAHPLPIWTPA

Important features of the protein:

Transmembrane domain:

amino acids 21-40 and 84-105 (type II)

FIGURE 11

GGCGCCGCGTAGGCCCGGGAGGCCGGGCCGGGCTGCGAGCGCCTGCCCCATGCGCCGC
CGCCTCTCCGCACG**ATG**TTCCCCCTCGCGGAGGAAAGCGGCGCAGCTGCCCTGGGAGGACGGC
AGGTCCGGGTTGCTCTCCGGCGGCCTCCCTCGGAAGTGTTCCGTCTTCCACCTGTTCTGTTGGC
CTGCCTCTCGCTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGG
CCCGGGCAGTCAGGGGACAAGGGCAGGAGACCTCGGGCCCTCCCCGTGCCTGCCCCCAGAG
CCGCCCCCTGAGCACTGGGAAGAAGACGCATCCTGGGGCCCCACCGCCTGGCAGTGCTGGT
GCCCTTCCGCGAACGCTTCGAGGAGCTCCTGGTCTTCGTGCCCCACATGCGCCGCTTCCTGA
GCAGGAAGAAGATCCGGCACCACATCTACGTGCTCAACCAGGTGGACCACTTCAGGTTCAAC
CGGGCAGCGCTCATCAACGTGGGCTTCCTGGAGAGCAGCAACAGCACGGACTACATTGCCAT
GCACGACGTTGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTTCCTGAGGCTGGGC
CCTTCCACGTGGCCTCCCCGGAGCTCCACCCTCTCTACCACTACAAGACCTATGTCGGCGGC
ATCCTGCTGCTCTCCAAGCAGCACTACCGGCTGTGCAATGGGATGTCCAACCGCTTCTGGGG
CTGGGGCCGCGAGGACGACGAGTTCTACCGGCGCATTAAGGGAGCTGGGCTCCAGCTTTTCC
GCCCCCTCGGGAATCACAACCTGGGTACAAGACATTTGCCCACCTGCATGACCCAGCCTGGCGG
AAGAGGGACCAGAAGCGCATCGCAGCTCAAAAACAGGAGCAGTTCAAGGTGGACAGGGAGGG
AGGCCTGAACACTGTGAAGTACCATGTGGCTTCCCGCACTGCCCTGTCTGTGGGCGGGGCC
CCTGCACTGTCCTCAACATCATGTTGGACTGTGACAAGACCGCCACACCCTGGTGACATTC
AGCT**TGA**GCTGGATGGACAGTGAGGAAGCCTGTACCTACAGGCCATATTGCTCAGGCTCAGGA
CAAGGCCTCAGGTCGTGGGCCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCA
AGCTACGCAATTGCAGCCACCCGGCCGCCAAGGCAGGCTTGGGCTGGGCCAGGACACGTGGG
GTGCCTGGGACGCTGCTTGCCATGCACAGTGATCAGAGAGAGGCTGGGGTGTGTCTGTCCG
GGACCCCCCTGCCTTCCTGCTCACCTACTCTGACCTCCTTCACGTGCCCAGGCCTGTGGG
TAGTGGGGAGGGCTGAACAGGACAACCTCTCATCACCTACTCTGACCTCCTTCACGTGCCC
AGGCCTGTGGGTAGTGGGGAGGGCTGAACAGGACAACCTCTCATCACCCCCAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 12

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56531

><subunit 1 of 1, 327 aa, 1 stop

><MW: 37406, pI: 9.30, NX(S/T): 1

MFPSRRKAAQLPWEDGRSGLLSGGLPRKCSVFHLFVACLSLGGFFSLLWLQLSCSGDVARAVR
GQGQETSGPPRACPPEPPPEHWEEDASWGPHRLAVLVPFRERFEELLVFVPHMRRFLSRKKI
RHHIYVLNQVDHFRFNRAALINVGFLSSNSTDYIAMHDVDLLPLNEELDYGFPEAGPFHVA
SPELHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDDEFYRRIKGAGLQLFRPSGI
TTGYKTFRHLHDPAWRKRDQKRIAAQKQEQFKVDREGGLNTVKYHVASRTALSVGGAPCTVL
NIMLDCDKTATPWCTFS

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 29-49 (type II)

N-glycosylation site.

amino acids 154-158

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 27-31

Tyrosine kinase phosphorylation site.

amino acids 226-233

N-myristoylation site.

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

FIGURE 13

CAATGTTTGCCTATCCACCTCCCCAAGCCCCTTTACCT**ATG**CTGCTGCTAACGCTGCTGCT
GCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCCAGAAAGTCT
CTTCTGCCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCCTTTCTGTGTCTC
CTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGT
GGGGGATGGC**TAA**GAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGG
GCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGC
CCTGTTCATTAAGAAATTGTTCCCTTCCCCTGTGTTCAATGTTTGTAAAGATTGTTCTGTGT
AAATATGTCTTTATAATAAACAGTTAAAAGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

13/249

FIGURE 14

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56862

<subunit 1 of 1, 73 aa, 1 stop

<MW: 7879, pI: 7.21, NX(S/T): 0

MLLLTLLLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQAQ
PRGEGEKVGDG

Important features:**Signal peptide:**

amino acids 1-15

Growth factor and cytokines receptors family:

amino acids 3-18

14/249

FIGURE 15

GGGACCCATGCGGCCGTGACCCCGGCTCCCTAGAGGCCAGCGCAGCCGCAGCGGACAAAG
 GAGCATGTCCGCGCCGGGGAAGGCCCGTCTCCGGCCGCCATAAGGCTCCGGTCGCCGCTGG
 GCCGCGCCGCGCTCCTGCCCGCCGGGCTCCGGGGCGGCCCGCTAGGCCAGTGCGCCGCCG
 CTCGCCCCGCAGGCCCGGCCCGCAGC**ATGG**AGCCACCCGGACGCCGGCGGGGGCCGCGCGCA
 GCCGCCGCTGTTGCTGCCGCTCTCGCTGTTAGCGCTGCTCGCGCTGCTGGGAGGCGGCGGCG
 GCGGCGGCGCCGCGGCGCTGCCCGCCGGCTGCAAGCACGATGGGCGGCCCGAGGGGCTGGC
 AGGGCGGCGGGCGCCGCGGAGGGCAAGGTGGTGTGCAGCAGCCTGGAACCTCGCGCAGGTCTT
 GCCCCAGATACTCTGCCCAACCGCACGGTCACCCCTGATTCTGAGTAACAATAAGATATCCG
 AGCTGAAGAATGGCTCATTTTCTGGGTAAAGTCTCCTTGAAAGATTGGACCTCCGAAACAAT
 CTTATTAGTAGTATAGATCCAGGTGCCTTCTGGGGACTGTCATCTCTAAAAAGATTGGATCT
 GACAAACAATCGAATAGGATGTCTGAATGCAGACATATTTGAGGACTCACCAATCTGGTTC
 GGCTAAACCTTTTCGGGGAATTTGTTTTCTTCATTATCTCAAGGAACCTTTTGATTATCTTGCG
 TCATTACGGTCTTTGGAATTCAGACTGAGTATCTTTTGTGTGACTGTAACATACTGTGGAT
 GCATCGCTGGGTAAAGGAGAAGAACATCACGGTACGGGATACCAGGTGTGTTTATCCTAAGT
 CACTGCAGGCCCAACCAGTCACAGGCGTGAAGCAGGAGCTGTTGACATGCGACCCCTCCGCTT
 GAATTGCCGTCTTTCTACATGACTCCATCTCATCGCCAAGTTGTGTTTGAAGGAGACAGCCT
 TCCTTTCCAGTGCATGGCTTCATATATTGATCAGGACATGCAAGTGTGTTGTTATCAGGATG
 GGAGAATAGTTGAAACCGATGAATCGCAAGGTATTTTTGTTGAAAAGAACATGATTCACAAC
 TGCTCCTTGATTGCAAGTGCCCTAACCATTTCTAATATTCAGGCTGGATCTACTGGAATTG
 GGGCTGTGATGTCCAGACCAAACGTGGGAATAATACGAGGACTGTGGATATTGTGGTATTAG
 AGAGTTCTGCACAGTACTGTCTCCAGAGAGGGTGGTAAACAACAAAGGTGACTTCAGATGG
 CCCAGAACATTGGCAGGCATTACTGCATATCTGCAGTGTACGCGGAACACCCATGGCAGTGG
 GATATATCCCGGAAACCCACAGGATGAGAGAAAAGCTTGGCGCAGATGTGATAGAGGTGGCT
 TTTGGGCAGATGATGATTATTCTCGCTGTCAGTATGCAATGATGTCACTAGAGTTCTTTAT
 ATGTTTAATCAGATGCCCTCAATCTTACCAATGCCGTGGCAACAGCTCGACAGTTACTGGC
 TTACACTGTGGAAGCAGCCAACTTTTCTGACAAAATGGATGTTATATTTGTGGCAGAAATGA
 TTGAAAAATTTGGAAGATTTACCAAGGAGGAAAAATCAAAAGAGCTAGGTGACGTGATGGTT
 GACATTGCAAGTAACATCATGTTGGCTGATGAACGTGTCTGTGGCTGGCGCAGAGGGAAGC
 TAAAGCCTGCAGTAGGATTGTGCAGTGTCTTCAGCGCATTGCTACCTACCGGCTAGCCGGTG
 GAGCTCACGTTTATTCAACATATTCACCCAATATTGCTCTGGAAGCTTATGTCATCAAGTCT
 ACTGGCTTCACGGGGATGACCTGTACCGTGTTCAGAAAAGTGGCAGCCTCTGATCGTACAGG
 ACTTTCGGATTATGGGAGGCGGGATCCAGAGGGGAAACCTGGATAAGCAGCTGAGCTTTAAGT
 GCAATGTTTCAAATACATTTTCGAGTCTGGCACTAAAGGTATGTTACATTCTGCAATCATTT
 AAGACTATTTACAGT**TAA**ATTAGAATGCTCCAAATGTTCTGCTTCGCAAAATAACCTTATTA
 AAAGATTTTTTTTTTGCAAGGAAGATAGGTATTATTGCTTTTGTACTGTTTTAAAGAAAACCTA
 ACCAGGAAGAACTGCATTACGACTTTCAAGGGCCCTAGGCATTTTTGCCTTTGATTCCCTTT
 CTTACATAAAAAATATCAGAAATTACATTTTATAACTGCAGTGGTATAAATGCAAATATACT
 ATTGTTACATGTGAAAAAATTTTATTTGACTTAAAAGTTTATTTATTTGTTTTTTTGTCTCCT
 GATTTTAAGACAATAAGATGTTTTTCATGGGCCCTAAAAGTATCATGAGCCTTTGGCACTGC
 GCCTGCCAAGCCTAGTGGAGAAGTCAACCTGAGACCAGGTGTTTAAATCAAGCAAGCTGTAT
 ATCAAAATTTTTGGCAGAAAACACAAATATGTCATATATCTTTTTTTAAAAAAAGTATTTCA
 TTGAAGCAAGCAAAATGAAAGCATTTTTACTGATTTTTAAAAATTGGTGCTTTAGATATATTT
 GACTACACTGTATTGAAGCAAAATAGAGGAGGCACAACTCCAGCACCTAATGGAACCACATT
 TTTTTCACCTTAGCTTTCTGTGGGCATGTGTAATTGTATTCTCTGCGGTTTTTAATCTCACAG
 TACTTTATTTCTGTCTTGCTCCCTCAATAATATCACAAACAATATTCCAGTCATTTTAATGGC
 TGCATAATAACTGATCCAACAGGTGTTAGGTGTTCTGGTTTAGTGTGAGCACTCAATAAATA
 TTGAATGAATGAACGAAAAAAAAAAAAAAAAA

FIGURE 16

MEPPGRRRRGRAQPPLLLPLSLLALLALLGGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK
VVCSSLELAQVLPDPTLPNRTVTLLISNNKISELKNGSFSGLSLLERLDLRNNLISSIDPGA
FWGLSSLKRLDLTNNRIGCLNADIFRGLTNLVRNLNSGNLFSSLSQGTFDYLASLRSLEFQT
EYLLCDCNILWMHRWVKEKNITVRDTRCVYPKSLQAQPVTGVKQELLTCDPPELEPSFYMTF
SHRQVVFEGDSLFPQCMASYIDQDMQVLWYQDGRIVETDESQGIFVEKNMIHNCSLIASALT
ISNIQAGSTGNWGCHVQTKRGNNTRTVDIVVLESSAQYCPPERVVNNKGDWRPRTLAGITA
YLQCTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDDYSRCQYANDVTRVLYMFNQMPNLN
TNAVATARQLLAYTVEAANFSDKMDVIFVAEMIEKFGRFTKEEKSKELGDMVDIASNIMLA
DERVLWLAQREAKACSRIVQCLQRIATYRLAGGAHVYSTYSPNIALEAYVIKSTGFTGMTCT
VFQKVAASDRTGLSDYGRRDPEGNLDKQLSFKCNVSNTFSSSLALKVCYILQSFKTIYS

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 13-40 (type II)

N-glycosylation site.

amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336,
433-437, 453-457, 592-596

N-myristoylation site.

amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57,
57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326,
384-390, 403-409, 554-560

FIGURE 17

GCGTGGGGATGTCTAGGAGCTCGAAGGTGGTGCTGGGCCTCTCGGTGCTGCTGACGGCGGCC
ACAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTAT
CAGAGACATTGAGAGGCAAATTCGGAAAAAAGAAAACATTCGTCTTTTGGGAGAACAGATTA
TTTTGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAGGATCTCAAAAA
TCATTGACTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTGTTGAT
GGAGAGTAGCTTAGTAGTATCTTCATCTTTTTTTTTTGGTCACTGTCCTTTTAAACTTGATCA
AATAAAGGACAGTGGGTCATATAAGTTACTGCTTTCAGGGTCCCTTATATCTGAATAAAGGA
GTGTGGGCAGACACTTTTTTGAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGG
TCACTGTCCAGTGCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGA
TGGATAGTAGCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACA
TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGAGGGAGAGACGCTCCTGATCGTCGAATCC

17/249

FIGURE 18

MSRSSKVVVLGLSVLLTAATVAGVHVKQQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT
EQLEAEREKMLLAKGSQKS

Signal peptide:

amino acids 1-21

MSRSSKVVVLGLSVLLTAATVAGVHVKQQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT
EQLEAEREKMLLAKGSQKS

FIGURE 19

CTGTCTGCTCTTTGCTTCAGCCGAGTCGCCACTGGCTGCCTGAGGTGCTCTTACAGCCTGTTCCAAAGTGTGGCTTAATCCGTCTCCACCACCAGATCTTTCTCCGTGGATTCTCTGCTAAGACCGCTGCC**ATG**CCAGTGACGGTAACCCGCACCACCATCACAACCACCACGACGTCATCTTCGGGCCTGGGGTCCCCCATGATCGTGGGGTCCCCTCGGGCCCTGACACAGCCCCTGGGTCTCCTTCGCTGCTGCAGCTGGTGTCTACCTGCGTGGCCTTCTCGCTGGTGGCTAGCGTGGGCGCCTGGACGGGGTCCATGGGCAACTGGTCCATGTTACCTGGTGCTTCTGCTTCTCCGTGACCTGATCATCCTCATCGTGGAGCTGTGCGGGCTCCAGGCCCGCTTCCCCCTGTCTTGGCGCAACTTCCCCATCACCTTCGCCTGCTATGCGGGCCTCTTCTGCCTCTCGGCCTCCATCATCTACCCCACCACCTATGTCCAGTTCCTGTCCCACGGCCGTTTCGCGGGACCACGCCATCGCCGCCACCTTCTTCTCCTGCATCGCGTGTGTGGCTTACGCCACCGAAGTGGCCTGGACCCGGGGCCCGGCCCGGCGAGATCACTGGCTATATGGCCACCGTACCCGGGCTGCTGAAGGTGCTGGAGACCTTCGTTGCCTGCATCATCTTCGCGTTCATCAGCGACCCCAACCTGTACCAGCACCAGCCGGCCCTGGAGTGGTGCGTGGCGGTGTACGCCATCTGCTTCATCCTAGCGGCCATCGCCATCCTGCTGAACCTGGGGGAGTGCACCAACGTGCTACCCATCCCCTTCCCAGCTTCCTGTGGGGCTGGCCTTGCTGCTGTGTCCTCCTCTATGCCACCGCCCTTGTTCTCTGGCCCCCTCTACCAGTTCGATGAGAAGTATGGCGGCCAGCCTCGGCGCTCGAGAGATGTAAGCTGCAGCCGCAGCCATGCCTACTACGTGTGTGCCTGGGACCGCCGACTGGCTGTGGCCATCCTGACGGCCATCAACCTACTGGCGTATGTGGCTGACCTGGTGCACCTCTGCCCACCTGGTTTTTGTCAAGGTC**TAA**ACTCTCCCAAGAGGCTCCCGTTCCCTCTCCAACCTCTTTGTTCTTCTTGCCCGAGTTTTCTTTATGGAGTACTTCTTTCTCCGCTTTCTCCTCTGTTTTTCTCTTCCCTGCTCTCCCTCCCTCCCACCTTTTTCTTTCTTTCTCCATTCCTTGCACTCTAACCAGTTCCTGGATGCATCTTCTTCCCTTCCCTTCTCCTTGCTGTTCCTTCCCTGTGTTGTTTTGTTGCCCACATCCTGTTTTACCCCTGAGCTGTTTCTCTTTTTCTTTCTTTCTTTTTTTTTTTTTTTTTTTTTTAAGACGGATTCTCACTCTGTGGCCCAGGCTGGAGTGCAGTGGTGCGATCTCAGCTCACTGCAACCCCCGCCTCCTGGGTCAAGCGATTCTCCTCCCAGCCTCCCAAGTAGCTGGGAGGACAGGTGTGAGCTGCCGCACCCAGCCTGTTTCTCTTTTCCACTCTTCTTTTTTCTCATCTCTTTTCTGGGTGTCCTGTGCGCTTTCTTATCTGCCTGTTTTGCAAGCACCTTCTCCTGTGTCCTTGGGAGCCCTGAGACTTCTTTCTCTCCTTGCCCTCCACCTCCAAAGGTGCTGAGCTCACATCCACACCCCTTGAGCCGTCCATGCCACAGCCCCCAAGGGGGCCCCATTGCCAAAGCATGCCTGCCACCCCTCGCTGTGCCTTAGTCAGTGTGTACGTGTGTGTGTGTGTGTGTGTGTTTTGGGGGGTGGGGGGTGGGTAGCTGGGGATTGGGGCCCTCTTTCTCCAGTGGAGGAAGGTGTGCAGTGTACTTCCCCCTTTAAATTAAAAACATATATATATATATATTTTGGAGGTCAGTAATTTCCAATGGGCGGGAGGCATTAAAGCACCGACCTGGGTCCCTAGGCCCGCCTGGCACTCAGCCTTGCCAGAGATTGGCTCCAGAATTTTGGCAGGCTTACAGAACACCACTGCCTAGAGGCCATCTTAAAGGAAGCAGGGGCTGGATGCCTTTCATCCCAACTATTCTCTGTGGTATGAAAAAG

FIGURE 20

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727

<subunit 1 of 1, 322 aa, 1 stop

<MW: 35274, pI: 8.57, NX(S/T): 1

MPVTVTRTTITTTTTSSSGLGSPMIVGSPRALTQPLGLLRLLQLVSTCVAFSLVASVGAWTG
SMGNWSMFTWCFCFSVTLLIILIVELCGLQARFPLSWRNFPI TFACYAALFCLSASIIYPTTY
VQFLSHGRSRDHAI AATFFSCIACVAYATEVAWTRARPGEITGYMATVPGLLKVLETFVACI
IFAFISDPNLYQHQP ALEWCVAVYAICFILAAIAILLNLGECTNVLPIPFPSFLSGLALLSV
LLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRRLAVAILTAINLLAYVAD
LVHSAHLVFVKV

Important features:**Transmembrane domains:**

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192,
205-226, 235-255 and 294-312

N-glycosylation site.

amino acids 66-69

Glycosaminoglycan attachment site.

amino acids 18-21

[illegible]

FIGURE 22

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSSLAQVNLSPFVSHPKVHMDPNYCHPSTSLHLCS
LAWSFTRLHPPLSPGISQVVKDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPAALSAFSSY
SDLSEGEQEARFAAGVAEQFAIAEAKLRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLG
PHLQDLFTGHRFSRPVRQGSVEPESDCSQTVPDTLCSSLCSLEDGLLGSPARLASQLLGDE
LLLAKLPPSRESAFRSLGPLEAQDSLNSPLTESCLSPAEEEEPAPCKDCQPLCPPLTGSWER
QRQASDLASSGVVSLDEDEAEPEEQ

Signal peptide:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232,
285-289, 324-328

Tyrosine kinase phosphorylation site.

amino acids 44-52

N-myristoylation site.

amino acids 17-23, 26-32, 173-179

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 11-22

FIGURE 23

GGTTCCTGGGCGCTCTGTTACACAAGCAAGATACAGCCAGCCCCACCTAATTTTGTTCCT
GGCACCCCTCCTGCTCAGTGCGACATTGTCACACTTAACCCATCTGTTTTCTCTAATGCACGA
CAGATTCCCTTCAGACAGGACAACCTGTGATATTTAGTTCCCTGATTGTAAATACCTCCTAAG
CCTGAAGCTTCTGTTACTAGCCATTGTGAGCTTCAGTTTCTTCATCTGCAAAATGGGCATAA
TACAATCTATTCTTGCCACATCAAGGGATTGTTATTCCTTTAAAAAAAACCAATACCAAAG
AAGCCTACA**ATG**TTGGCCTTAGCCAAAATTCTGTTGATTTCAACGTTGTTTTATTCACTTCT
ATCGGGGAGCCATGGAAAAGAAAATCAAGACATAAACACAACACAGAACATTGCAGAAGTTT
TAAAACAATGGAAAATAAACCTATTTCTTTGGAAAGTGAAGCAAACCTAAACTCAGATAAA
GAAAATATAACCACCTCAAATCTCAAGGCGAGTCATTCCCCTCCTTTGAATCTACCCAACAA
CAGCCACGGAATAACAGATTTCTCCAGTAACTCATCAGCAGAGCATTCTTTGGGCAGTCTAA
AACCCACATCTACCATTTCCACAAGCCCTCCCTTGATCCATAGCTTTGTTTCTAAAGTGCCT
TGGAATGCACCTATAGCAGATGAAGATCTTTTGCCCATCTCAGCACATCCCAATGCTACACC
TGCTCTGTCTTCAGAAAACCTTCACTTGGTCTTTGGTCAATGACACCGTGAAAACCTCTGATA
ACAGTTCCATTACAGTTAGCATCCTCTCTTCAGAACCAACTTCTCCATCTGTGACCCCTTG
ATAGTGGAACCAAGTGGATGGCTTACCACAAACAGTGATAGCTTCACTGGGTTTACCCCTTA
TCAAGAAAAACAACCTCTACAGCCTACCTTAAAATTCACCAATAATTCAAAACTCTTTCCAA
ATACGTCAGATCCCCAAAAGAAAATAGAAATACAGGAATAGTATTCGGGGCCATTTTAGGT
GCTATTCTGGGTGTCTCATTGCTTACTCTTGTGGGCTACTTGTGTGTGGAAAAGGAAAAC
GGATTCATTTTCCCATCGGCGACTTTATGACGACAGAAATGAACCAGTTCTGCGATTAGACA
ATGCACCGGAACCTTATGATGTGAGTTTTGGGAATTCTAGCTACTACAATCCAACCTTGAAT
GATTCAGCCATGCCAGAAAGTGAAGAAAATGCACGTGATGGCATTCCCTATGGATGACATACC
TCCACTTCGTACTTCTGTAT**TAGA**ACTAACAGCAAAAAGGCGTTAAACAGCAAGTGTCATCTA
CATCCTAGCCTTTTGACAAATTCATCTTTCAAAGGTTACACAAAATTACTGTCACGTGGAT
TTTGTCAAGGAGAATCATAAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCAT
CCAAAGGTTTTCTTTCTTACAATTTTTGGCCATCCTGAGGCATTTACTAAGTAGCCTTAATT
TGTATTTTAGTAGTATTTTCTTAGTAGAAAATATTTGTGGAATCAGATAAAACTAAAAGATT
TCACCATTACAGCCCTGCCTCATAACTAAATAATAAAAATTATTCCACCAAAAAATTCTAAA
ACAATGAAGATGACTCTTTACTGCTCTGCCTGAAGCCCTAGTACCATAATTCAAGATTGCAT
TTTCTTAAATGAAAATTGAAAGGGTGCTTTTTTAAAGAAAATTTGACTTAAAGCTAAAAAGAG
GACATAGCCCAGAGTTTCTGTTATTGGGAAATTGAGGCAATAGAAATGACAGACCTGTATTC
TAGTACGTTATAATTTTCTAGATCAGCACACACATGATCAGCCCACTGAGTTATGAAGCTGA
CAATGACTGCATTCAACGGGGCCATGGCAGGAAAGCTGACCCTACCCAGGAAAGTAATAGCT
TCTTTAAAGTCTTCAAAGGTTTTGGGAATTTTAACTTGTCTTAATATATCTTAGGCTTCAA
TTATTTGGGTGCCTTAAAAACTCAATGAGAATCATGGT

FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732

><subunit 1 of 1, 334 aa, 1 stop

><MW: 36294, pI: 4.98, NX(S/T): 13

MLALAKILLISTLFYSLLSGSHGKENQDINTTQNI AEVFKTMENKPISLESEANLNSDKENI
TTSNLKASHSPPLNLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPLIHSFVSKVPWNA
PIADEDLLPISAHPNATPALSSENFTWSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVE
PSGWLTTNSDSFTGFTPYQEKTTLQPTLKFTNNSKLPNTSDPQKENRNTGIVFGAILGAIL
GVSLTLVGYLLCGKRKTDSFSHRRLYDDRNEPVLRLDNAPEPYDVSFGNSSYYNPTLND
SA
MP ESEENARDGIPMDDIPPLRTSV

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 235-262

N-glycosylation site.

amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,
163-167, 218-222, 225-229, 298-302, 307-311

FIGURE 25

AACAGGATCTCCTCTTGCAGTCTGCAGCCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGC
 AGCCCGAAGATTCACT**ATG**GTGAAAATCGCCTTCAATACCCCTACCGCCGTGCAAAAGGAGG
 AGGCGCGGCAAGACGTGGAGGCCCTCCTGAGCCGCACGGTCAGAACTCAGATACTGACCGGC
 AAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCCTCTGGGAGATGTATGCTTACTCT
 CTTAGGCCTTTTCATTCATCTTGGCAGGACTTATTGTTGGTGGAGCCTGCATTTACAAGTACT
 TCATGCCCAAGAGCACCATTTACCGTGGAGAGATGTGCTTTTTTGATTCTGAGGATCCTGCA
 AATTCCCTTCGTGGAGGAGAGCCTAACTTCCTGCCTGTGACTGAGGAGGCTGACATTCGTGA
 GGATGACAACATTGCAATCATTGATGTGCCTGTCCCCAGTTTCTCTGATAGTGACCCTGCAG
 CAATTATTCATGACTTTGAAAAGGGAATGACTGCTTACCTGGACTTGTTGCTGGGGAACCTGC
 TATCTGATGCCCCCTCAATACTTCTATTGTTATGCCTCCAAAAAATCTGGTAGAGCTCTTTGG
 CAAACTGGCGAGTGGCAGATATCTGCCTCAAACCTTATGTGGTTCGAGAAGACCTAGTTGCTG
 TGGAGGAAATTCGTGATGTTAGTAACCTTGGCATCTTTATTTACCAACTTTGCAATAACAGA
 AAGTCCTTCGCGCTTCGTGCGAGAGACCTCTTGCTGGGTTTCAACAAACGTGCCATTGATAA
 ATGCTGGAAGATTAGACACTTCCCCAACGAATTTATTGTTGAGACCAAGATCTGTCAAGAG**T**
AAGAGGCAACAGATAGAGTGTCTTGGTAATAAGAAGTCAGAGATTTACAATATGACTTTAA
 CATTAAGGTTTATGGGATACTCAAGATATTTACTCATGCATTTACTCTATTGCTTATGCTTT
 AAAAAAAGGAAAAAAAAAAAAAAAACTACTAACCCTGCAAGCTCTTGTCAAATTTTAGTTTAAAT
 TGGCATTGCTTGTTTTTTTGAACTGAAATTACATGAGTTTCATTTTTTCTTGCATTTATAG
 GGTTTAGATTTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAAATTCATCC
 GTTGTTTTTTTTGTTTGTGTTTTTTCTTTTCCTTTAAGTAAGCTCTTTATTCATCTTATG
 GTGGAGCAATTTTAAAATTTGAAATATTTTAAATTGTTTTTGAACTTTTTGTGTAAAATATA
 TCAGATCTCAACATTGTTGGTTTCTTTTGTGTTTTTCATTTTGTACAACTTTCTTGAATTTAGA
 AATTACATCTTTGCAGTTCCTGTTAGGTGCTCTGTAATTAACCTGACTTATATGTGAACAATT
 TTCATGAGACAGTCATTTTAACTAATGCAGTGATTCTTCTCACTACTATCTGTATTGTGG
 AATGCACAAAATTGTGTAGGTGCTGAATGCTGTAAGGAGTTTAGGTTGTATGAATTCTACAA
 CCCTATAATAAATTTTACTCTATACAAAAAAAAAAAAAAAAAAAA

FIGURE 26

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828

<subunit 1 of 1, 263 aa, 1 stop

<MW: 29741, pI: 5.74, NX(S/T): 1

MVKIAFNTPTAVQKEEARQDVEALLSRTVVRTQILTGKELRVATQEKEGSSGRCMLTLLGLSF
ILAGLIVGGACIYKYFMPKSTIYRGEMCFFDSEDPANSLRGGEPNFLPVTEEADIREDDNIA
IIDVPVPSFSDSDPAAIHDFEKGMTAYLDLLLGNCYLMPLNTSIVMPPKNLVELFGKLASG
RYLPQTYVVREDLVAVEEIRDVSNLGIFIIYQLCNNRKSFRLRRRDLLLGFNKRAIDKCWKIR
HFPNEFIVETKICQE

Type II transmembrane domain:

amino acids 53-75

N-glycosylation site.

amino acids 166-170

Casein kinase II phosphorylation site.

amino acids 35-39, 132-136, 134-138

N-myristoylation site.

amino acids 66-72, 103-109

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 63-74

FIGURE 27

GGAGGAGGGAGGGCGGGCAGGCGCCAGCCCAGAGCAGCCCCGGGCACCAGCACGGACTCTCT
 CTTCCAGCCCAGGTGCCCCCACTCTCGCTCCATTTCGGCGGGAGCACCCAGTCCTGTACGCC
 AAGGAACTGGTCCTGGGGGCACCATGGTTTCGGCGGCAGCCCCAGCCTCCTCATCCTTCTG
 TTGCTGCTGCTGGGGTCTGTGCCTGCTACCGACGCCCCTGTGCCCCCTGAAGGCCACGTT
 CCTGGAGGATGTGGCGGGTAGTGGGGAGGCCGAGGGCTCGTCGGCCTCCTCCCCGAGCCTCC
 CGCCACCCTGGACCCCGGCCCTCAGCCCCACATCGATGGGGCCCCAGCCCACAACCCTGGGG
 GGCCCATCACCCCCACCAACTTCCTGGATGGGATAGTGGACTTCTTCCGCCAGTACGTGAT
 GCTGATTGCTGTGGTGGGCTCCCTGGCCTTTCTGCTGATGTTTCATCGTCTGTGCCGCGGTCA
 TCACCCGGCAGAAGCAGAAGGCCTCGGCCTATTACCCATCGTCCTTCCCCAAGAAGAAGTAC
 GTGGACCAGAGTGACCGGGCCGGGGGCCCCGGGCCTTCAGTGAGGTCCCCGACAGAGCCCC
 CGACAGCAGGCCCCGAGGAAGCCCTGGATTTCCTCCCGGCAGCTCCAGGCCGACATCTTGCCG
 CCACCCAGAACCTCAAGTCCCCCACCAGGGCTGCACTGGGCGGTGGGGACGGAGCCAGGATG
 GTGGAGGGCAGGGGCGCAGAGGAAGAGGAGAAGGGCAGCCAGGAGGGGGACCAGGAAGTCCA
 GGGACATGGGGTCCCAGTGGAGACACCAGAGGCGCAGGAGGAGCCGTGCTCAGGGGTCTTG
 AGGGGGCTGTGGTGGCCGGTGAGGGCCAAGGGGAGCTGGAAGGGTCTCTCTTGTTAGCCCAG
 GAAGCCCAGGGACCAGTGGGTCCCCCGAAAGCCCCTGTGCTTGCAGCAGTGTCCACCCCAG
 TGTCTAAAGTCCTCCCGGGCTGCCAGCCCTGACTGTGCGGGCCCCCAAGTGGTCACCTCCCC
 GTGTATGAAAAGGCCTTCAGCCCTGACTGCTTCCTGACACTCCCTCCTTGGCCTCCCTGTGG
 TGCCAATCCCAGCATGTGCTGATTCTACAGCAGGCAGAAATGCTGGTCCCCGGTGCCCCGGA
 GGAATCTTACCAAGTGCCATCATCCTTCACCTCAGCAGCCCCAAAGGGCTACATCCTACAGC
 ACAGCTCCCCTGACAAAGTGAGGGAGGGCACGTGTCCCTGTGACAGCCAGGATAAAACATCC
 CCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGTGCCCGGCCCAAACCTACTTTTTTAAACA
 GCTACAGGGTAAAATCCTGCAGCACCCACTCTGGAAAATACTGCTCTTAATTTTCCTGAAGG
 TGGCCCCCTGTTTCTAGTTGGTCCAGGATTAGGGATGTGGGGTATAGGGCATTAAATCCTC
 TCAAGCGCTCTCCAAGCACCCCCGGCCTGGGGGTGAGTTTCTCATCCCGCTACTGCTGCTGG
 GATCAGGTTGAATGAATGGAACCTTCCTGTCTGGCCTCCAAGCAGCCTAGAAGCTGAGGG
 GCTGTGTTTGAGGGGACCTCCACCCTGGGGAAGTCCGAGGGGCTGGGGAAGGGTTTCTGACG
 CCCAGCCTGGAGCAGGGGGGCCCTGGCCACCCCCTGTTGCTCACACATTGTCTGGCAGCCTG
 TGTCCACAATATTCGTCAGTCCTCGACAGGGAGCCTGGGCTCCGTCTGCTTTAGGGAGGCT
 CTGGCAGGAGGTCCTCTCCCCCATCCCTCCATCTGGGGCTCCCCAACCTCTGCACAGCTCT
 CCAGGTGCTGAGATATAATGCACCAGCACATAAACCTTTATTCCGGCCTGAAAAAAAAAAAA
 AAAGA

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FIGURE 28

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852

><subunit 1 of 1, 283 aa, 1 stop

><MW: 29191, pI: 4.52, NX(S/T): 0

MVSAAAPSLILLILLLLLLGSPATDARSVPLKATFLEDVAGSGEAEAGSSASSPSLPPPWTPAL
SPTSMGPQPTTLGGPSPPTNFLDGIVDFFRQYVMLIAVVGSLAFLLMFIVCAAVITRQKQKA
SAYYPSSFPPKKKYVDQSDRAGGPRAFSEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSP
TRAALGGGDGARMVEGRGAEEEEKGSQEGDQEVQGHGVPVETPEAQEEPCSGVLEGAVVAGE
GQGELEGSLLLAQEAQGPVGPPEPCACSSVHPSV

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 94-118

N-myristoylation site.

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,
211-217, 238-244, 242-248

FIGURE 29

[illegible]

FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212

><subunit 1 of 1, 440 aa, 1 stop

><MW: 42208, pI: 6.36, NX(S/T): 1

MKFQGPLACLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGA
 AGSKVSEALGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG
 ADAVRGSWQGVPGHSGAWETSGGHGIFGSQGGGLGGQGQGNPGGLGTPWVHGYPGNSAGSFGM
 NPQGAPWQGQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGSGGGSSNSGGGS
 GSQSGSSGSGSNGDNNNGSSSGSSSGSSSGSSSGSSSGSSSGSSSGNSGGSRGDSGSESSW
 GSSTGSSSGNHGGSGGGNGHKPGCEKPGNEARGSGESGIQGFRGQGVSSNMREISKEGNRLL
 GSGDNYRGQGSWSGGGDAVGGVNTVNSETSPGMFNFDTFWKNFKSKLGFINWDAINKDQ
 RSSRIP

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,
 74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,
 155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,
 218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,
 249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,
 279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,
 295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,
 323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,
 383-389, 387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

FIGURE 30

FIGURE 31

GACCGGTCCCTCCGGTCTGGATGTGCGGACTCTGCTGCAGCGAGGGCTGCAGGCCCGCCGGGCGGTGCTCACCG
 TGCCCTGGCTGGTGGAGTTTCTCTCCTTTGCTGACCATGTTGTTCCCTTGCTGGAATATTACCGGGACATCTTCA
 CTCTCCTGCTGCGCCTGCACCGGAGCTTGGTGTGTGTCGAGGAGAGTGAGGGGAAGATGTGTTTCTGAACAAGC
 TGCTGCTACTTGCTGTCTGGGCTGGCTTTTCCAGATTCCACAGTCCCTGAGGACTTGTTCTTTCTGGAAGAGG
 GTCCCTCATATGCCTTTGAGGTGGACACAGTAGCCCCAGAGCATGGCTTGACAATGCGCCTGTGGTGGACCAGC
 AGCTGCTCTACACCTGCTGCCCTACATCGGAGAGCTCCGGAAACTGCTCGCTTCGTGGGTGTGAGGCAGTAGTG
 GACGGAGTGGGGGCTTCATGAGGAAAATCACCCCCACCACTACCACCAGCCTGGGAGCCCAGCCTTCCCAGACCA
 GCCAGGGGCTGCAGGCACAGCTCGCCAGCCCTTTTCCACAACCAGCCGCCCTCCTTGCGCCGAGCCGTAGAGT
 TCGTGGCAGAAAGAATTGGATCAAACCTGTGTCAAACATATCAAGGCTACACTGGTGGCAGATCTGGTGCGCCAGG
 CAGAGTCACTTCTCCAAGAGCAGCTGGTGACACAGGGAGAGGAAGGGGGAGACCCAGCCCAGCTGTTGGAGATCT
 TGTGTTCCCAGCTGTGCCCTCACGGGGCCCAGGCATTGGCCCTGGGGCGGGAGTTCTGTCAAAGGAAGAGCCCTG
 GGGCTGTGCGGGCGCTGCTTCCAGAGGAGACCCCGGCAGCCGTTCTGAGCAGTGACAGAAACATTGCTGTGGGGC
 TTGCAACAGAGAAAGCCTGTGCTTGGCTGTGAGCCAACATCACAGCACTGATCAGGAGGGAGGTGAAAGCAGCAG
 TGAGTCGCACACTTCGAGCCCAGGGTCTGAACTGCTGCCCGGGGGAGCGGAGGGGCTGCTCCCGCGCCTGAGC
 GTGCTCTCCTTGGCCGTGGGGCCACGGGACCCTGACGAGGGAGTCTCCCCAGAGCATCTGGAACAGCTCCTAGGC
 CAGCTGGGGCAGACGCTGCGGTGCCGCCAGTTCTGTGCCCACTGCTGAGCAGCATCTGGCAAAGTGCTCTGTG
 GAGTTAGCTTCCCTCCTCGTTGCAGATCAAATTCCTATCCTAGGGCCCCCGGCACAGTACAGGCTGGAGAGAGGG
 CAGGCTCGAAGGCTTCTGCACATGCTGCTTTCCTTGTGGAAGGAAGACTTTCAGGGGCCGTTCCGCTGCAGCTG
 CTGCTGAGCCCAAGAAATGTGGGGCTTCTGGCAGACACAAGGCCAAGGGAGTGGGACTTGCTGCTATTCTTGCTA
 CGGGAGCTGGTGGAGAAGGGTCTGATGGGACGGATGGAGATAGAGGCCTGCCTGGGCAGCCTCCACCAGGCCCAG
 TGGCCAGGGGACTTGTGCTGAAGAATTAGCAACACTGTCTAATCTGTTTCTAGCCGAGCCCCACCTGCCAGAACC
 CAGCTAAGAGCCTGTGAGTTGGTGCAGCCAAACCGGGGCACTGTGCTGGCCCAGAGCTAGGGCTGAGAAGTGGCC
 CTGCCCTTGGGCATTGCACCAGAACCCTGGACCCCCGCTCACGAGGAGGCCCAAGTGCCCAATGCAGACCCTCAC
 TGGTTGGGGTGTAGCTGGGTCTACAGTCAGACTTCCTGCTCTAAGGGTGTCACTGCCTGGCATCCCACCACGCGA
 ATCCTAGAGGAAGGAGAGTTGGCCTGATTTGGGATTATGGCAGAAAAGTCCAGAGATGCCAGTCTGGAGTAGAA
 GAGGTGGTGTGTTTATCTCTTGGATACTAAATGAAATGAGGTGTGTGGGCTTGTCAACACAGAATTCAAGCCT
 CATTTGCTATCCCAGCATCTCTTAAACTTTGTAGTCTTGGAATTCATGACAGAGGCAAATGACTCCTGCTTAAC
 TTATGAAGAAAGTTAAACATGAATCTTGGGAGTCTACATTTTCTTATCACCAGGAGCTGGACTGCCATCTCCTT
 ATAAATGCCTAACACAGGCCGGGTCTGGTGGCTCATGCCTGTAATCCCAGCACTTTGAGAGGCCTGAGGTGCGCG
 GACTGCCTGAGGTGAGGAATTCAGAGCCAGCCTGGCCAACATGGCAAAACCCATCTCTACTAAAAATAAAAAAA
 TTATTAGCTGGGCATGGTGGTGTGTGCTGTAATCCCAGCTACTCAGGAGGATGAGGCAGGAGACCTGCTTGAAC
 CTGGAGGTGGAGTTGCAGTGAGCCGAGGTGCGACCACTGCACTCCAGTCTGGGTAACAGAGCGAGACTTTCTAG
 AAAAAAGCCTAACAAACAGATAAGGTAGGACTCAACCAACTGAAACCTGACTTTCCCCCTGTACCTTCAGCCCCCTG
 TGCAGGTAGTAACCTCTTGAGACCTCTCCCTGACCAGGGACCAAGCACAGGGCATTTAGAGCTTTTTTAGAATAAA
 CTGGTTTTCTTTAAAAAAGGGCTTTTATTTAAAAATTTCTCCCCACACGATGGCTCCTGCAATCTGCCACAGCTC
 TGGGGCGTGTCTGTAGGGAAAGGCCCTGTTTTCCCTGAGGCGGGGCTGGGCTTGTCCATGGGTCCGCGGAGCTG
 GCCGTGCTTGGCGCCCTGGCGTGTGTCTAGCTGCTTCTTGCCGGGCACAGAGCTGCGGGGTCTGGGGGCACCGGG
 AGCTAAGAGCAGGCTCTGGTGCAGGGGTGGAGGCCTGTCTTAACCGACACCCTGAGGTGCTCCTGAGATGCTG
 GGTCCACCCTGAGTGGCACGGGGAGCAGCTGTGGCCGGTGTCTCTCYTAGGCCAGTCTGGGGAAACTAAGCTC
 GGGCCCTTCTTGCAAAGACCGAGGATGGGTGGGTGTGGGGGACTCATGGGGAATGGCCTGAGGAGCTACGTGT
 GAAGAGGGCGCCGTTTGTGGCTGCAGCGCCTGGAGCGCCTCTCTCCTGAGCCTCAGTTTCCCTTTCCGTCTA
 ATGAAGAACATGCCGTCTCGGTGTCTCAGGGCTATTAGGACTTGCCTCAGGAAGTGGCCTTGGACGAGCGTCAT
 GTTATTTTCACAACTGTCTGCGACGTTGGCTGGGCACGTGATGGAATGGCCCATGTCCCTCTGCTGCGTGGAC
 GTCGCGGTGCGGAGTGCGCAGCCAGAGGCGGGGCAGACGTGCGCCTGGGGGTGAGGGGAGGGCGCCCCGGGAGGG
 CCTCACAGGAAGTTGGGCTCCCGCACCACCAGGCAGGGCGGGCTCCCGCCGCGCCGCCGCCACCACCGTCCAGG
 GGCCGCTAGACAAAGTGGAAGTTCGCGCTTGGGCTCGCTGCGCAGCAGGTAGCCCTTGATGCAGTGCGGCAGCGCG
 TCGTCCGCCAGCTGGAAGCAGCGCCCGTCCACCAGCACGAACAGCCGGTGCAGCCT

FIGURE 32

MCFLNKLALLLAVLGWLFQIPTVPEDLFFLEEGPSYAFEVDTVAPEHGLDNAPVVDQQLLYTC
CPYIGELRKLLASWVSGSSGRSGGFMRKITPTTTTSLGAQPSQTSQGLQAQLAQAFFHNQPP
SLRRTVEFVAERIGSNCVKHIKATLVADLVRQAESLLQEQLVTQGEEGGDPQQLLEILCSQL
CPHGAQALALGREFCQRKSPGAVRALLPEETPAAVLSSAENIAVGLATEKACAWLSANITAL
IRREVKAAVSRTLRAQGPEPAARGERRGCSRA

Signal peptide:

amino acids 1-18

N-glycosylation site.

amino acids 244-248

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 89-93

Casein kinase II phosphorylation site.

amino acids 21-25, 167-171, 223-227

N-myristoylation site.

amino acids 100-106, 172-178, 207-213

Microbodies C-terminal targeting signal.

amino acids 278-282

FIGURE 33

TCCCTTGACAGGTCTGGTGGCTGGTTCGGGGTCTACTGAAGGCTGTCTTGATCAGGAACTG
 AAGACTCTCTGCTTTTGCCACAGCAGTTCCTGCAGCTTCCTTGAGGTGTGAACCCACATCCC
 TGCCCCCAGGGCCACCTGCAGGACGCCGACACCTACCCCTCAGCAGACGCCGGAGAGAA**ATG**
 AGTAGCAACAAAGAGCAGCGGTGAGCAGTGTTTCGTGATCCTCTTTGCCCTCATCACCATCCT
 CATCCTCTACAGCTCCAACAGTGCCAATGAGGTCTTCCATTACGGCTCCCTGCGGGGCCGTA
 GCCGCCGACCTGTCAACCTCAAGAAAGTGGAGCATCACTGACGGCTATGTCCCCATTCTCGGC
 AACAAAGACACTGCCCTCTCGGTGCCACCAAGTGTGTGATTGTGAGCAGCTCCAGCCACCTGCT
 GGGCACCAAGCTGGGGCCCTGAGATCGAGCGGGCTGAGTGTACAATCCGCATGAATGATGCAC
 CCACCACTGGCTACTCAGCTGATGTGGGCAACAAGACCACCTACCGCGTCGTGGCCCATTCC
 AGTGTGTTCCGCGTGCTGAGGAGGCCCCAGGAGTTTGTCAACCGGACCCCTGAAACCGTGT
 CATCTTCTGGGGGCCCCCGAGCAAGATGCAGAAGCCCCAGGGCAGCCTCGTGCGTGTGATCC
 AGCGAGCGGGCCTGGTGTTCCTCAACATGGAAGCATATGCCGTCTCTCCCGGCCGCATGCGG
 CAATTTGACGACCTCTTCCGGGGTGAGACGGGGCAAGGACAGGGAGAAAGTCTCATTCGTGGTT
 GAGCACAGGCTGGTTTACCATGGTGATCGCGGTGGAGTTGTGTGACCACGTGCATGTCTATG
 GCATGGTCCCCCCCCAACTACTGCAGCCAGCGGCCCGCCTCCAGCGCATGCCCTACCACTAC
 TACGAGCCCAAGGGGCCGGACGAATGTGTACCTACATCCAGAATGAGCACAGTCGCAAGGG
 CAACCACCACCGCTTCATCACCGAGAAAAGGGTCTTCTCATCGTGGGCCCAGCTGTATGGCA
 TCACCTTCTCCCACCCCTCCTGGACC**TAG**GCCACCCAGCCTGTGGGACCTCAGGAGGGTCA
 AGGAGAAGCAGCCTCCGCCCAGCCGCTAGGCCAGGGACCATCTTCTGGCCAATCAAGGCTTG
 CTGGAGTGTCTCCAGCCAATCAGGGCCTTGAGGAGGATGTATCCTCCAGCCAATCAGGGCC
 TGGGGAATCTGTTGGCGAATCAGGGATTTGGGAGTCTATGTGGTTAATCAGGGGTGTCTTTC
 TTGTGCAGTCAGGGTCTGCGCACAGTCAATCAGGGTAGAGGGGGTATTTCTGAGTCAATCTG
 AGGCTAAGGACATGTCTTTCCCATGAGGCCTTGGTTCAGAGCCCCAGGAATGGACCCCCCA
 ATCACTCCCCACTCTGCTGGGATAATGGGGTCTGTCCAAGGAGCTGGGAACTTGGTGTG
 CCCCCTCAATTTCCAGCACCCAGAAAGAGAGATTGTGTGGGGGTAGAAGCTGTCTGGAGGCC
 GGCCAGAGAATTTGTGGGGTTGTGGAGGTTGTGGGGGCGGTGGGGAGGTCCCAGAGGTGGGA
 GGCTGGCATCCAGGTCTTGGCTCTGCCCTGAGACCTTGGACAAACCCTTCCCCCTCTCTGGG
 CACCCTTCTGCCACACCAAGTTTCCAGTGCGGAGTCTGAGACCCTTCCACCTCCCCCTACAA
 GTGCCCTCGGGTCTGTCTCCCCGTCTGGACCCTCCCAGCCACTATCCCTTGCTGGAAGGCT
 CAGCTCTTTGGGGGGTCTGGGGTGACCTCCCCACCTCCTGGAAAACCTTTAGGGTATTTTTTC
 GCAAACCTCCTTCAGGGTTGGGGGACTCTGAAGGAAACGGGACAAAACCTTAAGCTGTTTTCT
 TAGCCCCCTCAGCCAGCTGCCATTAGCTTGGCTCTTAAAGGGCCAGGCCTCCTTTTCTGCCCT
 CTAGCAGGGAGGTTTTCCAACCTGTTGGAGGCGCCTTTGGGGCTGCCCTTTGTCTGGAGTCA
 CTGGGGGCTTCCGAGGGTCTCCCTCGACCCTCTGTCTGCTGGGATGGCTGTCTGGGAGCTGT
 ATCACCTGGGTCTGTCCCCTGGCTCTGTATCAGGCACTTTATTAAAGCTGGGCCTCAGTGG
 GGTGTGTTTGTCTCCTGCTCTTCTGGAGCCTGGAAGGAAAGGGCTTCAGGAGGAGGCTGTGA
 GGCTGGAGGGACCAGATGGAGGAGGCCAGCAGCTAGCCATTGCACACTGGGGTGATGGGTGG
 GGGCGGTGACTGCCCCAGACTTGGTTTTGTAATGATTTGTACAGGAATAAACACACCTACGC
 TCCGGAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 34

MSSNKEQRSADFVILFALITILILYSSNSANEVFHYGSLRGRSRPVLKKWSITDGYVPIL
GNKTLPSRCHQCVIVSSSSHLLGTLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAH
SSVFRVLRRPQEFVNRTPETVFIFWGPPSKMQKPQGS�VRVIQRAGLVFPNMEAYAVSPGRM
RQFDDLFRGETGKDREKSHSWLSTGWFTMVIAVELCDHVHVYGMVPPNYCSQRPRLQRMPIH
YYEPKGPDECVTYIQNEHSRKGNHHRFITEKRVFSSWAQLYGITFSHPSWT

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 9-31 (type II)

N-glycosylation site.

amino acids 64-68, 115-119

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 50-54

Casein kinase II phosphorylation site.

amino acids 3-7, 29-33, 53-57, 197-201

Tyrosine kinase phosphorylation site.

amino acids 253-262

N-myristoylation site.

amino acids 37-43, 114-120, 290-294

GTTCTCATAGTTTGGCGTCTCTAAAGGAAAAACACTAAAATGAGGAACTCAGCGGACCGGGAGCGACGCACTT
 GAGGGAAGCATCCCTAGCTGTGGCGCAGAGGGGCGAGGCTGAAGCCGAGTGGCCCGAGGTGTCTGAGGGGCTGG
 GCGAAAGGTGAAAGAGTTTCAAGAACAGCTTCTTGGAAACCATGACCCATGAAGTCTTGTCGACATTTATACCGT
 CTGAGGTAGCAGCTCGAAACTAGAAGAGTGGAGTGTGGCAGGACGCGCATCTCTTTGTGTATCCCTGGC
 GGCTATGGGACGTTGGCTTCAGACCTTTGTGATACACC**ATG**CTGCGTGGGACGATGACGGCGTGGAGAGGAATG
 AGGCGTGAAGTGCACACTGGCTTGGCTCCCTAGCCACAGCAGGCTGCTTTGCTGACTTGAACGAGGTCCCTCAG
 GTCACCGTCCAGCCTGCGCTCCACCGTCCAGAAAGCCCGGAGGCATGTGATCTTGGGCTGCGTGGTGGAACTCCA
 AGGATGAATGTAACCTGGCGCTGAATGGAAGAGACTGAATGGCTCGGATGATGCTCTGGGTGCTCATCAC
 CACGGGACCCCTCGTCATCACTGCCCTTAACAAACCACTGTGGGACGGTACCAGTGTGTGGCCGGATGCCTGCG
 GGGGCTGTGGCCAGCGTGCCAGCCACTGTGACACTAGCCAATCTCCAGGACTTCAAGTTAGATGTGCAGCACGT
 ATTGAAGTGGATGAGGGAACACAGCAGTCATTGCCCTGCCACCTGCCTGAGAGCCACCCCAAGGCCACAGGTCCGG
 TACAGCTCAACAAAGAGTGGCTGGAGGCTCCAGAGGTAACCTACCTGATCATGCCCTCAGGGAACCTCCAGATT
 GTGAATGCCAGCCAGGAGGACGAGGGCATGTACAAGTGTGCAGCCTACAACCCAGTGACCCAGGAAGTGAAGAAC
 TCCGGCTCCAGCGACAGGCTACGTGTGCGCCGCTCCACCGCTGAGGCTGCCCGCATCATCTACCCCCCAGAGGGC
 CAAACCATCATCGTACCAGGAGGCGAGAGTCTCATTTCTGGAGTGTGTGGCCAGTGGAATCCCACCCCCACGGGT
 ACCTGGGCAAGGATGGTCCAGTGTACCCGGCTACAACAAGACGCGCTTCTGCTGAGCAACCTCCTCATCGAC
 ACCACGAGGAGGAGACTCAGGCACCTACCGCTGCATGGCCGACAAATGGGTTGGGAGCCCGGGGCGAGCGGT
 ATCCTCTACAATGTCCAGGTGTTTGAACCCCCTGAGGTCAACATGGAGCTATCCAGCTGGTCTATCCCCCTGGGGC
 CAGAGTGCCAAAGCTTACCTGTGAGGTGCGTGGGAACCCCCCGCTCCGTGCTGTGGCTGAGGAATGCTGTGCC
 CTCTATCCAGCCAGCGCTCCGGCTCTCCCGCAGGGCCCTGCGCGTGCTCAGCATGGGGCTGAGGACGAAGG
 GTCTACCACTGCATGGCCGAGAAGAGTGTGGAGCGCCCATGCGGTAGTCCAGCTGCGGACCTCCAGGCCAAGC
 ATAACCCCAAGGCTATGGCAGGATGCTGAGCTGGCTACTGGCACACCTCCTGTATACCCCTCCAAACTCGGCAAC
 CCTGAGCAGATGCTGAGGGGGCAACCGCGCTCCCGAGACCCCAACCTCAGTGGGGCTGCTTCCCCGAAGTGT
 CCAGGAGAGAAGGGGCGAGGGGCTCCCGCGAGGCTCCCATCTCAGCTCGCCCCGACCTCCAGACAGAC
 TCATATGAACCTGGTGTGGCGGCTCGGCATGAGGGCAGTGGCCGGGCGCAATCCTCTACTATGTGGTGAACAC
 CGAAGCAGGTCAAAATTCCTCTGACGATTGGACCATCTCTGGCATTCAGCCAACCCAGCACCGCCTGACCCCT
 ACCAGACTTGACCCCGGAGCTGTATGAAGTGGAGTGGCAGCTTACAACGTGCGGGAGAGGGCCAGACAGCC
 ATGTCACCTTCGAACCTGGACGGCGCCCAACCCGAGATCATGGCCAGCAAGAGCAGAGATCCAGAGAGAG
 AACCCTGGAGCCAGTCCCAGAGCAGCAGCCAGCCAGACACCGCGCCTCTCCCCCAGAAGCTCCCGACAGG
 CCCACCATCTCCACGGCTCCGAGACCTCAGTGTACGTGACCTGGATTCCCCGTGGGAATGGTGGGTTCCTAATC
 CAGTCTTCCGTGTGGAGTACAAGAAGCTAAAGAAAGTGGGAGACTGGATTCTGGCCACCGAGCCCATCCCCCA
 TCGGGCTGTCCGTGGAGATCAGGGGCTAGAGAAAGGCACTTCTACAAGTTTCAGTCCGGCTCTGAACATG
 CTGGGGGAGAGCGAGCCAGCGCCCCCTCTCGGCCCTACGTGGTGTGGGCTACAGCGGTGCGGTGTACGAGAGG
 CCCGTGGCAGGTCTTATATCACCTTCACGGATGCGGTCAATGAGACCACCATCATGCTCAAGTGGATGTACATC
 CCAGCAAGTAAACAACAACCCCAATGCATGGCTTTTATATCTATTATCGACCCACAGACAGTGACAATGATAGT
 GACTACAAGAAGTATGTGTGAAGGGACAAGTACTGGCACTCCATCAGCCACCTGACAGCCAGAGACCTCCTAC
 GACATTAAGATGCAGTGCTTCAATGAAGGAGGGGAGCAGGTTCAGAACCTGATGATCTGTGAGACCAAGCT
 CGGAAGTCTTCTGGCCAGCCTGGTGCAGTCCACCCCCAACTCTGGCCCCACCACAGCCGCCCTTCTCTGAAACC
 ATAGAGCGGCGCGTGGGCATGGGGCCATGGTGGCTCGCTCCAGCGACCTGCCCTATCTGATTGTCTGGGGTCTGT
 CTGGGCTCCATCGTTTCATCATCTCACCTTATCCCCCTCTGCTGTGGAGGGCTGGTCTAAGCAAAAACAT
 ACAACAGACCTGGGTTTCTCTCGAAGTGGCTTCCACCTCTCGCCGTATACCTATGGTGCAATTGGGAGGACT
 CCAGGCCACCAGGCCAGTGGACAGCCCTACCTCAGTGGCATCAGTGGACGGGCTGTGCTAATGGGATCCACATG
 AATAGGGGCTCCCCCTCGGCTGCAGTGGGCTACCCGGCATGAAGCCCCAGCAGCACTGCCAGGCGAGCTTCAG
 CAGCAGGTGACACCAGCAGCCTGCTGAGGCACCCCATCTTGGCAATGGATATGACCCCAAAGTCAACAGATC
 ACAGAGGGGTCCCAAGTCTAGCCCGGACGAGGGCTTTTCTTATACACACTGCCGAGCACTCACTACAGGCTG
 CTGACGCCCCATCAGCACTGCTGCCAACGCCAGGAGCAGCCTGCTGCTGTGGCCAGTCAGGGGTGAGGAGAGCC
 CCCGACAGTCTGCTCTGGAAGCAGTGTGGGACCTCCATTTCTCACTCAGGGCCCCCATGCTGCTTGGGCTTGTG
 CCAGTTGAAGAGGTGGACAGTCTGACTCCTGCCAAGTGAGTGGAGGAGCTGGTGTCCCAGCACCCCGTAGGG
 GCCTACGTAGGACAGGAACCTGGAATGCAGCTCTCCCCGGGGCCTGGTGGCTGTCTTTTGAACACCAACCT
 CTCACAATT**TAG**GCAGAAGCTGATATCCAGAAAGACTATATATTGTTTTTTTTTAAAAAAGAGAAAAA
 AGAGACAGAGAAAAATGGTATTATTATTTTCTATTATAGCCATATTATATATTATGCACTTGTAAATAAATGTA
 TATGTTTTATAATTCTGGAGAGACATAAGGAGTCTACCCGTTTGGTGTGGAGAGGAAAAATAAGAGCTGCCA
 CCTAACAGGAGTCACCAGGAAAGCACCGCAGCAGGCTGGCGGGGACAGACTCTAAACCTGGGGCTCTGCAGTG
 GCAGGCGAGGCTGCAGGAGGCCACAGATAAGCTGGCAAGAGGAAGGATCCAGGCACATGGTTCTCACGAGCA
 TGAGGGAACAGAGAGGGGACAGGTATCACAGCTGGAGACACCCACAGATGGCTGGATCCGGTGTACGGGAA
 ACATTTTCTAAGATGCCATGAGAAGACACCAAGATGTGTACAGCACTATGAGCATTAATAAAACCTTCAGAA
 CAATAATCCGTGGCAACATATCTCTGTAAAAACAAACACTGTAACTTCTAATAAATGTTTGTCTCTCTGTAAAA

FIGURE 36

MLRGTMTAWRGM RPEVTLACLLLATAGCFADLNEVPQVTVQ PASTVQKPGGT VILGCVVEPP
 RMNV TWRLNGKELNGSDDALGVLITHGTLVIT ALNNHTVGRYQC VARMPAGAVASVPATVTL
 ANLQDFKLDVQH VIEVDEGNTAVIACHLPESH PKAQVRYSVKQEWLEASRGNYLIMP SGNLQ
 IVNASQEDEGMYKCAAYNPVTQEVKTS GSSDRLRVRRSTAEAAARI IYPPEAQTI IIVTKGQSL
 ILECVASGI PPRVTWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVGQPGA
 AVILYNVQVFEPPEVTMELS QLVIPWGQSAKLTCEVRGNPPPSVLWLRNAVPLISSQRLRLS
 RRALRVLSMGPEDEGVYQCMAENEVGS AHAVVQLRTSRPSITPRLWQDAELATGTPPVSPSK
 LGNPEQMLRGQPALPRPPTS VGPASPKCPGEKGQGA PAEAPIILSSPRTSKTDSYELVWRPR
 HEGSGRAPILYYVVKHRKQVTNSSDDWTISGIPANQHRLTLTRLDPGSLYEVEMAAYNCAGE
 GQTAMVTFRTGRRPKPEIMASKEQQIQRDDPGAS PQSSSQPDHGRLSPPEAPDRPTISTASE
 TSVYVTWIPRGNGGFPIQSFRVEYKKLKKVGDWILATSAIPPSRLSVEITGLEKGTSYKFRV
 RALNMLGESEPSAPSRPYVVS GYSGRVYERPVAGPYITFTDAVNETTIMLKWMIIPASNNNT
 PIHGFYIYYRPTDSDNDSYKKDMVEGD KYWHSISHLQ PETS YDIKMQCFNEGGESEFSNVM
 ICETKARKSSGQPGRLP PPTLAPPQPLPETIERPVGTGAMVARSSDLPYLIVGVVLGSIVL
 IIVTFIPFCLWRWSKQKHTTDLGFP RSALPPSCP YTMVPLGGLPGHQASGQPYLSGISGRA
 CANGIHMNRGCP SAAVGYPGMKPQQHCPGELQQQSDTSSLLRQTHLGNGYDPQSHQITRGPK
 SSPDEGSFLYTL PDDSTHQLLQPHHDCCQRQE QPAAVGQSGVRRAPDSPVLEAVWDP PFHSG
 PPCC LGLVPVEEVDSPDSCQVSGGDWCPQHPVGAYVGQEPGMQLSPGPLVRVSFETPPLTI

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 16-30 (type II), 854-879

FIGURE 37

CGGGAGGCTGGGTCGTCATGATCCGGACCCCATTTGTCGGCCTCTGCCCATCGCCTGCTCCTC
 CCAGGCTCCCGCGGCCGACCCCGCGCAAC**ATG**CAGCCCACGGGCGCGAGGGTTCCCGCGC
 GCTCAGCCGGCGGTATCTGCGGCGTCTGCTGCTCCTGCTACTGCTGCTGCTGCTGCGGCAGC
 CCGTAACCCGCGCGGAGACCACGCCGGGCGCCCCAGAGCCCTCTCCACGCTGGGCTCCCC
 AGCCTCTTCACCACGCCGGGTGTCCCCAGCGCCCTCACTACCCAGGCCTCACTACGCCAGG
 CACCCCCAAAACCCTGGACCTTCGGGGTCGCGCGCAGGCCCTGATGCGGAGTTTCCCACTCG
 TGGACGGCCACAATGACCTGCCCCAGGTCCTGAGACAGCGTTACAAGAATGTGCTTCAGGAT
 GTTAACCTGCGAAATTTTCAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGT
 GGGTGCCCAAGTTCTGGTCAGCCTCCGTCTCATGCCAGTCCCAGGACCAGACTGCCGTGCGCC
 TCGCCCTGGAGCAGATTGACCTCATTACCCGCATGTGTGCCTCCTACTCTGAACTCGAGCTT
 GTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAGCTGGCCTGCCTCATTGGCGTGNAGGG
 TGGTCACTCACTGGACAGCAGCCTCTCTGTGCTGCGCAGTTTCTATGTGCTGGGGGTGCGCT
 ACCTGACACTTACCTTCACCTGCAGTACACCATGGGCAGAGAGTTCCACCAAGTTCAGACAC
 CACATGTACACCAACGTCAGCGGATTGACAAGCTTTGGTGAGAAAGTAGTAGAGGAGTTGAA
 CCGCCTGGGCATGATGATAGATTTGTCTATGCATCGGACACCTTGATAAGAAGGGTCCTGG
 AAGTGTCTCAGGCTCCTGTGATCTTCTCCCACTCAGCTGCCAGAGCTGTGTGTGACAATTTG
 TTGAATGTTCCCGATGATATCCTGCAGCTTCTGAAGAACGGTGGCATCGTGATGGTGACACT
 GTCCATGGGGGTGCTGCAGTGCAACCTGCTTGCTAACGTGTCCACTGTGGCAGATCACTTTG
 ACCACATCAGGGCAGTCATTGGATCTGAGTTCATCGGGATTGGTGGAATTTATGACGGGACT
 GGCCGGTTCCCTCAGGGGCTGGAGGATGTGTCCACATACCCAGTCCTGATAGAGGAGTTGCT
 GAGTCGTASCTGGAGCGAGGAAGAGCTTCAAGGTGTCCTTCGTGGAAACCTGCTGCGGGTCT
 TCAGACAAGTGAAAAAGGTGAGAGAGGAGAGCAGGGCGCAGAGCCCCGTGGAGGCTGAGTTT
 CCATATGGGCAACTGAGCACATCCTGCCACTCCACCTCGTGCCCTCAGAATGGACACCAGGC
 TACTCATCTGGAGGTGACCAAGCAGCCAACCAATCGGGTCCCCTGGAGGTCCTCAAATGCCT
 CCCCATACCTTGTTCCAGGCCTTGTGGCTGCTGCCACCATCCCAACCTTCACCCAGTGGCTC
 TGCT**TGA**CACAGTCGGTCCCCGCGAGAGGTCACTGTGGCAAAGCCTCACAAAGCCCCCTCTCCT
 AGTTCATTCAACAAGCATATGCTGAGAATAAACATGTTACACATGGAAAA

FIGURE 38

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817

><subunit 1 of 1, 487 aa, 1 stop, 2 unknown

><MW: 53569.32, pI: 7.68, NX(S/T): 5

MQPTGREGSRALSRRYLRRLLLLLLLLLLLRQPVTRAETTPGAPRALSTLGSPSLFTTPGVPS
 ALTTPGLTTPGTPKTLDLRGRAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLRNFSHGQ
 TSLDRLRDGLVGAQFWSASVSCQSQDQTAVRLALEQIDLIHRMCASYSELELV TSAEGLNSS
 QKLACLIGVXGGHSLDSSLSVLRSFYVLGVRYLTLTFTCSTPWAESSTKFRHHMYTNVSGLT
 SFGEKVVEELNRLGMMIDLSYASDTLIRRVLEVSQAPVIFSHSAARAVCDNLLNVPDDILQL
 LKNGGIVMVTLSMGVLQCNNLANVSTVADHFDHIRAVIGSEFIGIGGNYDGTGRFPQGLEDV
 STYPVLIEELLSRXWSEEEELQGVLRGNLLRVFRQVEKVREESRAQSPVEAEFPYGQLSTSCH
 SHLVPQNGHQATHLEVTKQPTNRVPWRSSNASPYLVPGLVAAATIPFTTQWLC

Important features of the protein:

Signal peptide:

amino acids 1-36

Transmembrane domain:

amino acids 313-331

N-glycosylation sites.

amino acids 119-122, 184-187, 243-246 and 333-336

N-myristoylation sites.

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 136-146

FIGURE 39

TGCTAGGCTCTGTGTCCACAAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACACAGA
TCCCTCTATGACTGCAATGTGAGGTGTCCGGCTTTGCTGGCCCAGCAAGCCTGATAAGC**ATG**
AAGCTCTTATCTTTGGTGGCTGTGGTCTGGGTGTTTGCTGGTGCCCCAGCTGAAGCCAACAA
GAGTTCTGAAGATATCCGGTGCAAATGCATCTGTCCACCTTATAGAAACATCAGTGGGCACA
TTTACAACCAGAATGTATCCCAGAAGGACTGCAACTGCCTGCACGTGGTGGAGCCCATGCCA
GTGCCTGGCCATGACGTGGAGGCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAG
CACCACCACCATCAAGGTCATCATTTGTCATCTACCTGTCCGTGGTGGGTGCCCTGTTGCTCT
ACATGGCCTTCCTGATGCTGGTGGACCCTCTGATCCGAAAGCCGGATGCATACACTGAGCAA
CTGCACAATGAGGAGGAGAATGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCATCCCTCGG
GGGACCCCGAGCAAACACAGTCCTGGAGCGTGTGGAAGGTGCCCAGCAGCGGTGGAAGCTGC
AGGTGCAGGAGCAGCGGAAGACAGTCTTCGATCGGCACAAGATGCTCAGC**TAGAT**GGGCTGG
TGTGGTTGGGTCAAGGCCCCAACACCATGGCTGCCAGCTTCCAGGCTGGACAAAGCAGGGGG
CTACTTCTCCCTTCCCTCGGTTCCAGTCTTCCCTTTAAAGCCTGTGGCATTTTTTCTCCTT
CTCCCTAACTTTAGAAATGTTGTACTTGGCTATTTTGATTAGGGAAGAGGGATGTGGTCTCT
GATCTCTGTTGTCTTCTTGGGTCTTTGGGGTTGAAGGGAGGGGGGAAGGCAGGCCAGAAGGGA
ATGGAGACATTCGAGGCGGCCTCAGGAGTGGATGCGATCTGTCTCTCCTGGCTCCACTCTTG
CCGCTTCCAGCTCTGAGTCTTGGGAATGTTGTTACCTTGGAAGATAAAGCTGGGTCTTCA
GGAACTCAGTGTCTGGGAGGAAAGCATGGCCCAGCATTACGCATGTGTTCCCTTTCTGCAGTG
GTTCTTATCACACCTCCCTCCCAGCCCCGGCGCCTCAGCCCCAGCCCCAGCTCCAGCCCTG
AGGACAGCTCTGATGGGAGAGCTGGGCCCCCTGAGCCCACTGGGTCTTCAGGGTGCCTGGA
AGCTGGTGTTCGCTGTCCCCTGTGCACTTCTCGCACTGGGGCATGGAGTGCCCATGCATACT
CTGCTGCCGGTCCCCTCACCTGCACCTGAGGGGTCTGGGCAGTCCCTCCTCTCCCCAGTGTC
CACAGTCACTGAGCCAGACGGTTCGGTTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGAA
CACCACAGCCCCTGTACTTGGGTTGCCTCTTGTCCCTGAACTTCGTTGTACCAGTGCATGGA
GAGAAAATTTTGTCTCTTGTCTTAGAGTTGTGTGTAAATCAAGGAAGCCATCATTAATTTG
TTTTATTTCTCTCA

FIGURE 40

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278

<subunit 1 of 1, 183 aa, 1 stop

<MW: 20574, pI: 6.60, NX(S/T): 3

MKLLSLVAVVGCLLVPPAEANKSSEDIRCKCICPPYRNISGHIYNQNVSQKDCNCLHVVEPM
PVPGHDVEAYCLLCECRYEERSTTTIKVIIIVYLSVVGALLLYMAFLMLVDPLIRKPDAYTE
QLHNEEENEDARSMAAAAASLGGPRANTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 90-112

N-glycosylation sites.

amino acids 21-24, 38-41 and 47-50

FIGURE 41

AGCGGGTCTCGCTTGGGTTCCGCTAATTTCTGTCTGAGGCGTGAGACTGAGTTCATAGGGTCTGGGTCCCCGA
 ACCAGGAAGGGTTGAGGGAAACAATCTGCAAGCCCCCGCAGCCCAAGTGAGGGGCCCCGTGTTGGGGTCTCCC
 TCCCTTTGCATTCCCACCCCTCCGGGCTTTCGCTCTTCTGGGGACCCCTCGCCGGGAGATGCGCGCTTGATG
 CGGAGCAAGGATTTCGTCTGCTGCCTGCTCCTACTGGCCGCGGTGCTGATGGTGGAGAGCTCACAGATCGGCAGT
 TCGCGGGCCAACTCACTCCATCAAGTCTCTCTGGGCGGGGAGACGCCTGGTCAGGCCGCCAATCGATCTGCG
 GGCATGTACCAAGGACTGGCATTCGGCGGCAGTAAGAAGGGCAAAAACCTGGGGCAGGCCTACCTTGTAGCAGT
 GATAAGGAGTGTGAAGTTGGGAGGTATTGCCACAGTCCCCACCAAGGATCATCGGCCTGCATGGTGTGTGGAGA
 AAAAGAAGCGCTGCCACCGAGATGGCATGTGCTGCCCCAGTACCCGCTGCAATAATGGCATCTGTATCCCAGTT
 ACTGAAAGCATCTTAACCCCTCACATCCCGGCTCTGGATGGTACTCGGCACAGAGATCGAAACCACGGTCATTAC
 TCAAACCATGACTTGGGATGGCAGAATCTAGGAAGACCACACACTAAGATGTCACATATAAAAGGGCATGAAGGA
 GACCCCTGCCTACGATCATCAGACTGCATTGAAGGGTTTTGCTGTGCTCGTCATTTCTGGACCAAATCTGCAA
 CCAGTGCTCCATCAGGGGGAAGTCTGTACCAAACAACGCAAGAAGGGTTCTCATGGGCTGGAAATTTTCCAGCGT
 TCGCATGTGCGAAGGGCCTGTCTGCAAAGTATGGAAGATGCCACCTACTCCTCAAAGCCAGACTCCATGTG
 TGTGAGAAAATTTGATCACCATTGAGGAACATCATCAATTGCAGACTGTGAAGTTGTGTATTTAATGCATTATAG
 CATGGTGGAAAATAAGGTTTCAGATGCAGAAGATGGCTAAAATAAGAAACGTGATAAGAATATAGATGATCACA
 AAAGGGAGAAAGAAAACATGAATGAATAGATTAGAATGGGTGACAAATGCAGTGCAGCCAGTGTTCATTATG
 CACTTGTCTATGTAAATAATGTACACATTTGTGGAAAATGCTATTATTAAGAGAACAAGCACACAGTGGAAATT
 ACTGATGAGTAGCATGTGACTTTCCAAGAGTTTAGGTTGTGCTGGAGGAGAGGTTTCTTCAGATTGCTGATTGC
 TTATACAAATAACCTACATGCCAGATTTCTATTCAACGTTAGAGTTTAAACAAATACTCCTAGAATAACTTGTTA
 TACAATAGGTTCTAAAAATAAAATTTGCTAAACAAGAAATGAAAACATGGAGCATTGTTAATTTACAACAGAAAAT
 TACCTTTTGATTGTAACTACTTCTGCTGTTCAATCAAGAGTCTTGGTAGATAAGAAAAAATCAGTCAATAT
 TTCAAATAAATGCAAATAATGGCCAGTTGTTTAGGAAGGCCTTTAGGAAGACAAATAAATAACAAACAACAG
 CCACAAATACTTTTTTTCAAATTTTAGTTTTACCTGTAATTAATAAGAACTGATACAAGACAAAAACAGTTCC
 TTCAGATTCTACGGAATGACAGTATATCTCTTTATCCTATGTGATTCTCTGCTCTGAATGCATTATATTTCCA
 AACTATACCCATAAATTTGTGACTAGTAAATACTTACACAGAGCAGAATTTTCACAGATGGCAAAAAAATTTAA
 GATGTCCAATATATGTGGGAAAAGAGCTAACAGAGAGATCATTATTTCTTAAAGATTGGCCATAACCTATATTTT
 GATAGAATTAGATTGGTAAATACATGTATTATACATACTCTGTGGTAATAGAGACTTAAGCTGGATCTGTACTG
 CACTGGAGTAAGCAAGAAAATTTGGGAAAACCTTTTTCGTTTTGTTTCAGGTTTTGGCAACACATAGATCATATGCTG
 AGGCACAAGTTGGCTGTTTCATCTTTGAAACCAGGGGATGCACAGTCTAAATGAATATCTGCATGGGATTTGCTAT
 CATAATATTTACTATGCAGATGAATTCAGTGTGAGGTCTGTGTCCGTACTATCCTCAAATATTTATTTTATAG
 TGCTGAGATCCTCAAATAATCTCAATTTCAAGAGGTTTCACAAAATGTACTCCTGAAGTAGACAGAGTAGTGAGG
 TTTCAATTGCCCTCTATAAGCTTCTGACTAGCCAATGGCATCATCCAATTTTCTTCCCAAACCTCTGCAGCATCTG
 CTTTATTTGCCAAAGGGCTAGTTTCGGTTTTCTGCAGCCATTGCGGTTAAAAAATATAAGTAGGATAACTTGTA
 ACCTGCATATTGCTAATCTATAGACACCACAGTTTCTAAATTTCTTTGAAACCACTTTACTACTTTTTTTAACTT
 AACTCAGTTCTAAATACCTTTGTCTGGAGCACAAAACAATAAAAGGTTATCTTATAGTCGTGACTTTAACTTTTG
 TAGACCACAATTCATTTTTAGTTTTCTTTTACTTAAATCCCCTCTGCAGTCTCAAATTTAAGTTCTCCCAGTAG
 AGATTGAGTTTGAGCCTGTATATCTATTAAAAATTTCACTTCCCACATATATTTACTAAGATGATTAAGACTTA
 CATTTTCTGCACAGGTCTGCAAAAACAAAAATTATAAACTAGTCCATCCAAGAACCAGTTTGTATAAACAGGT
 TGCTATAAGCTTGTGAAATGAAATGGAACATTTCAATCAAACATTTCTATATAACAATTATTATATTTACAAT
 TTGGTTTTCTGCAATATTTTCTTATGTCCACCTTTTAAAAATTATTATTTGAAGTAATTTATTTACAGGAAATG
 TTAATGAGATGTATTTCTTATAGAGATATTTCTTACAGAAAGCTTTGTAGCAGAATATATTTGCAGCTATTGAC
 TTTGTAATTTAGGAAAAATGTATAATAAGATAAAATCTATTAAATTTTTCTCCTCTAAAAACTGAAAAA
 AAAAAAAAAAAAAAAAAA

FIGURE 42

MAALMRSKDSSCCLLLLA AVL MV E S S Q I G S S R A K L N S I K S S L G G E T P G Q A A N R S A G M Y Q G L A
F G G S K K G K N L G Q A Y P C S S D K E C E V G R Y C H S P H Q G S S A C M V C R R K K K R C H R D G M C C P S T R C N N
G I C I P V T E S I L T P H I P A L D G T R H R D R N H G H Y S N H D L G W Q N L G R P H T K M S H I K G H E G D P C L R S
S D C I E G F C C A R H F W T K I C K P V L H Q G E V C T K Q R K K G S H G L E I F Q R C D C A K G L S C K V W K D A T Y S
S K A R L H V C Q K I

Signal peptide:

amino acids 1-25

MAALMRSKDSSCCLLLLA AVL MV E S S Q I G S S R A K L N S I K S S L G G E T P G Q A A N R S A G M Y Q G L A
F G G S K K G K N L G Q A Y P C S S D K E C E V G R Y C H S P H Q G S S A C M V C R R K K K R C H R D G M C C P S T R C N N
G I C I P V T E S I L T P H I P A L D G T R H R D R N H G H Y S N H D L G W Q N L G R P H T K M S H I K G H E G D P C L R S
S D C I E G F C C A R H F W T K I C K P V L H Q G E V C T K Q R K K G S H G L E I F Q R C D C A K G L S C K V W K D A T Y S
S K A R L H V C Q K I

FIGURE 43

TCTCAATCTGCTGACCTCGTGATCCGCTGACCTTGTAATCCACCTACCTTGGCCTCCCAAA
GTGTTGGGATTACAGGCGTGAGCCACCGCGCCCGGCCAACATCACGTTTTTAAAAATTGATT
TCTTCAAATTCATGGCAAATATTTCCCTTCCCTTTAACTTCTTATGTCAGAATGAGGAAGGA
TAGCTGCATTTATTTAGTCAGTTTTCATTGCATAGTAATATTTTCATGTAGTATTTTCTAAG
TTATATTTTAGTAATTCATATGTTTTAGATTATAGGTTTTAACATACTTGTGAAAATACTTG
ATGTGTTTTTAAAGCCTTGGGCAGAAATTCTGTATTGTTGAGGATTTGTTCTTTTATCCCCCT
TTTAAAGTCATCCGTCCTTGGCTCAGGATTTGGAGAGCTTGCACCACCAAAAATGGCAAACA
TCACCAGCTCCCAGATTTTGGACCAGTTGAAAGCTCCGAGTTTGGGCCAGTTTACCACCACC
CCAAGTACACAGCAGAATAGTACAAGTCACCCTACAAC TACTACTTCTTGGGACCTCAAGCC
CCCAACATCCCAGTCCTCAGTCCTCAGTCATCTTGACTTCAAATCTCAACCTGAGCCATCCC
CAGTTCTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCACTGTTCTCTCT
CCTGGTTTTGGAGTCCTTTCCCTTCCCAGGCCAAACTTCGAGAATCAACACCTGGAGACAGTCC
CTCCACTGTGAACAAGCTTTTGCAGCTTCCCAGCACGACCATTGAAAATATCTCTGTGTCTG
TCCACCAGCCACAGCCCAAACACATCAAACCTTGCTAAGCGGCGGATACCCCCAGCTTCTAAG
ATCCCAGCTTCTGCAGTGGAAATGCCTGGTTCAGCAGATGTCACAGGATTAAATGTGCAGTT
TGGGGCTCTGGAATTTGGGTCAGAACCTTCTCTCTCTGAATTTGGATCAGCTCCAAGCAGTG
AAAATAGTAATCAGATTCCCATCAGCTTGTATTCGAAGTCTTTAAGTGAGCCTTTGAATACA
TCTTTATCAATGACCAGTGCAGTACAGAACTCCACATATACAAC TCCGTCATTACCTCCTG
CAGTCTGACAAGCTCATCACTGAATTCTGCTAGTCCAGTAGCAATGTCTTCCTCTTATGACC
AGAGTTCTGTGCATAACAGGATCCCATACCAAAGCCCTGTGAGTTCATCAGAGTCAGTCCA
GGAACCATCATGAATGGACATGGTGGTGGTTCGAAGTCAGCAGACACTAGACAGTAAGTATAG
CAGCAAGCTACTCTTGTCATGGCTGGTGCCAACCAAACAGAGGAAGAGGATAGCTCACGTGA
TGTGGAAAACACCAGTTGGTCAATGGCTCATTTCGT**TAAA**AAGCAGCCCTTTTGCTTTTTTGT
TTTTGGACCAGGTGTTGGCTGTGGTGTATTAGAAATGTCTTAACCACAGCAAGAAGGAGGT
GGTGGTCTCATATTCTTTCTGCCCTAATCAGACTGCACCACAAGTGCAGCATA CAGTATGCAT
TTTAAAGATGCTTGGGCCAGGCGGGGTGGCTGATGCCCAT AATCCCAGTGCTTTGGGGGGCC
AAGGCAGGCAGATTGCCCAAGCTCAGGAGTTTGAGACCACCCTGGGCAACATGGTGAAACTC
TGTCTCTACTAAAATACGAAAAACTAGCCGGGTGTGGTGGCGGCGCGTGCCTGTAATCCCAG
CTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGGCTACAAAGTGAGACTCC
GTCTGAAAAGA

FIGURE 44

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTT
PSTQQNSTSHPTTTTSDWDLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAQVTVPP
PGLEFSPSQAKLRESTPGDSPSTVNKLLQLPSTTIENISVSVHQPPKHIKLAKRRIPPASK
IPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAPSSSENSNQIPISLYSKSLSEPLNT
SLSMTSAVQNSTYTTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIYQSPVSSSESAP
GTIMNGHGGGRSQQTLDSKYSSKLLLSWLVP TKQRKRIAHVMWKTPVGQWLIR

Signal peptide:

amino acids 1-24

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FIGURE 45

GCCGAGTGGGACAAAGCCTGGGGCTGGGCGGGGGCC**ATG**GCGCTGCCATCCCGAATCCTGCT
 TTGGAAACTTGTGCTTCTGCAGAGCTCTGCTGTTCTCCTGCACTCAGCGGTGGAGGAGACGG
 ACGCGGGGCTGTACACCTGCAACCTGCACCATCACTACTGCCACCTCTACGAGAGCCTGGCC
 GTCCGCCTGGAGGTCACCGACGGCCCCCGGCCACCCCGCCTACTGGGACGGCGAGAAGGA
 GGTGCTGGCGGTGGCGCGCGGCGCACCCGCGCTTCTGACCTGCGTGAACCGCGGGCACGTGT
 GGACCGACCGGCACGTGGAGGAGGCTCAACAGGTGGTGCCTGGGACCGGCAGCCGCCCCGGG
 GTCCCGCACGACCGCGCGGACCGCCTGCTGGACCTCTACGCGTCGGGCGAGCGCCGCGCCTA
 CGGGCCCCCTTTTTCTGCGCGACCGCGTGGCTGTGGGCGCGGATGCCTTTGAGCGCGGTGACT
 TCTCACTGCGTATCGAGCCGCTGGAGGTGCGCGACGAGGGCACCTACTCCTGCCACCTGCAC
 CACCATTACTGTGGCCTGCACGAACGCCGCGTCTTCCACCTGACGGTCGCGGAACCCACGC
 GGAGCCGCCCCCGGGGCTCTCCGGGCAACGGCTCCAGCCACAGCGGCGCCCCAGGCCACG
 ACCCCACACTGGCGCGCGGCCACAACGTCATCAATGTCATCGTCCCCGAGAGCCGAGCCAC
 TTCTTCCAGCAGCTGGGCTACGTGCTGGCCACGCTGCTGCTCTTCATCCTGCTACTGGTCAC
 TGTCTCTCTGGCCGCCCGCAGGCGCCGCGGAGGCTACGAATACTCGGACCAGAAGTCGGGAA
 AGTCAAAGGGGAAGGATGTTAACTTGGCGGAGTTCGCTGTGGCTGCAGGGGACCAGATGCTT
 TACAGGAGTGAGGACATCCAGCTAGATTACAAAAACAACATCCTGAAGGAGAGGGCGGAGCT
 GGCCACAGCCCCCTGCCTGCCAAGTACATCGACCTAGACAAAGGGTTCCGGAAGGAGAACT
 GCAAA**TAG**GGAGGCCCTGGGCTCCTGGCTGGGCCAGCAGCTGCACCTCTCCTGTCTGTGCTC
 CTCGGGGCATCTCCTGATGCTCCGGGGCTCACCCCCCTTCCAGCGGCTGGTCCCGCTTTCT
 GGAATTTGGCCTGGGCGTATGCAGAGGCCGCTCCACACCCCTCCCCAGGGGCTTGGTGGC
 AGCATAGCCCCCACCCTGCGGCCTTTGCTCACGGGTGGCCCTGCCACCCCTGGCACAAACC
 AAAATCCCCTGATGCCATCATGCCCTCAGACCCTTCTGGGCTCTGCCCCGCTGGGGGCTG
 AAGACATTCTGGAGGACACTCCCATCAGAACCTGGCAGCCCCAAAACCTGGGGTCAGCCTCA
 GGGCAGGAGTCCCACTCCTCCAGGGCTCTGCTCGTCCGGGGCTGGGAGATGTTCTGGAGGA
 GGACACTCCCATCAGAACTTGGCAGCCTTGAAGTTGGGGTCAGCCTCGGCAGGAGTCCCACT
 CCTCCTGGGGTGCTGCCTGCCACCAAGAGCTCCCCACCTGTACCACCATGTGGGACTCCAG
 GCACCATCTGTTCTCCCCAGGGACCTGCTGACTTGAATGCCAGCCCTTGCTCCTCTGTGTTG
 CTTTGGGCCACCTGGGGCTGCACCCCTGCCCTTTCTCTGCCCCATCCCTACCCTAGCCTTG
 CTCTCAGCCACCTTGATAGTCACTGGGCTCCCTGTGACTTCTGACCCTGACACCCCTCCCTT
 GGACTCTGCCTGGGCTGGAGTCTAGGGCTGGGGCTACATTTGGCTTCTGTACTGGCTGAGGA
 CAGGGGAGGGAGTGAAGTTGGTTTGGGGTGGCCTGTGTTGCCACTCTCAGCACCCACATTT
 GCATCTGCTGGTGGACCTGCCACCATCACAATAAAGTCCCCATCTGATTTTTAAAAA
 AAAAA

FIGURE 46

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60618

<subunit 1 of 1, 341 aa, 1 stop

<MW: 38070, pI: 6.88, NX(S/T): 1

MALPSRILLWKLVLQSSAVLLHSAVEETDAGLYTCNLHHHYCHLYESLAVRLEVTDGPPAT
PAYWDGEKEVLAVARGAPALLTCVNRGHVWTD RHVEEAQQVVHWD RQPPGVPHDRADRLDL
YASGERRAYGPLFLRDRVAVGADAFERGFSLRIEPLVADEGTYSCHLHHHYCGLHERRVF
HLTVAEPHAEP PPRGSPGNGSSHSGAPGPDPTLARGHNVINVIVPESRAHFFQQLGYVLATL
LLFILLLVTVLLAARRRRGGYEYSDQKSGKSKGKDVNLAEFAVAAGDQMLYRSEDIQLDYKN
NILKERAELAHSPLPAKYIDL DKGFRKENCK

Important features:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 237-262

N-glycosylation site.

amino acids 205-208

Cell attachment sequence.

amino acids 151-154

Coproporphyrinogen III oxidase proteins.

amino acids 115-140

FIGURE 47

CGCCGGAGGCAGCGGCGGCGTGGCGCAGCGGCGAC**ATG**GCCGTTGTCTCAGAGGACGACTTT
CAGCACAGTTCAAACCTCCACCTACGGAACCACAAGCAGCAGTCTCCGAGCTGACCAGGAGGC
ACTGCTTGAGAAGCTGCTGGACCGCCCGCCCCCTGGCCTGCAGAGGCCCGAGGACCGCTTCT
GTGGCACATACATCATCTTCTTCAGCCTGGGCATTGGCAGTCTACTGCCATGGAACCTTCTTT
ATCACTGCCAAGGAGTACTGGATGTTCAAACCTCCGCAACTCCTCCAGCCCAGCCACCGGGGA
GGACCCTGAGGGGCTCAGACATCCTGAACTACTTTGAGAGCTACCTTGCCGTTGCCTCCACCG
TGCCCTCCATGCTGTGCCTGGTGGCCAACTTCTGCTTGTCAACAGGGTTGCAGTCCACATC
CGTGTCTTGGCCTCACTGACGGTCATCCTGGCCATCTTCATGGTGATAACTGCACTGGTGAA
GGTGGACACTTCCTCCTGGACCCGTTGGTTTTTTTTGCGGTCACCATTGTCTGCATGGTGATCC
TCAGCGGTGCCTCCACTGTCTTCAGCAGCAGCATCTACGGCATGACCGGCTCCTTTCCTATG
AGGAACTCCCAAGCACTGATATCAGGAGGAGCCATGGGCGGGACGGTCAGCGCCGTGGCCTC
ATTGGTGGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTTCTGACGG
CCACCATCTTCCTCGTGCTCTGCATGGGACTCTACCTGCTGCTGTCCAGGCTGGAGTATGCC
AGGTACTACATGAGGCCTGTTCTTGGCGGCCATGTGTTTTCTGGTGAAGAGGAGCTTCCCCA
GGACTCCCTCAGTGCCCTTTCGGTGGCCTCCAGATTGATTCCCACACACCCCTCTCC
GCCCCATCCTGAAGAAGACGGCCAGCCTGGGCTTCTGTGTACCTACGTCTTCTTCATCACC
AGCCTCATCTACCCCGCCGTCTGCACCAACATCGAGTCCCTCAACAAGGGCTCGGGCTCACT
GTGGACCACCAAGTTTTTCATCCCCCTCACTACCTTCTCCTGTACAACCTTTGCTGACCTAT
GTGGCCGGCAGCTCACCGCCTGGATCCAGGTGCCAGGGCCCAACAGCAAGGCGCTCCCAGGG
TTCGTGCTCCTCCGGACCTGCCTCATCCCCCTCTTCGTGCTCTGTAACCTACCAGCCCCGCGT
CCACCTGAAGACTGTGGTCTTCCAGTCCGATGTGTACCCCGCACTCCTCAGCTCCCTGCTGG
GGCTCAGCAACGGCTACCTCAGCACCCCTGGCCCTCCTCTACGGGCCTAAGATTGTGCCCAGG
GAGCTGGCTGAGGCCACGGGAGTGGTGATGTCCTTTTATGTGTGCTTGGGCTTAACACTGGG
CTCAGCCTGCTCTACCCTCCTGGTGCACCTCATC**TAGA**AAGGGAGGACACAAGGACATTGGTG
CTTCAGAGCCTTTGAAGATGAGAAGAGAGTGCAGGAGGGCTGGGGGCCATGGAGGAAAGGCC
TAAAGTTTCACTTGGGGACAGAGAGCAGAGCACACTCGGGCCTCATCCCTCCCAAGATGCCA
GTGAGCCACGTCCATGCCCATTCCGTGCAAGGCAGATATTCCAGTCATATTAACAGAACACT
CCTGAGACAGTTGAAGAAGAAATAGCACAAATCAGGGGTACTCCCTTCACAGCTGATGGTTA
ACATTCCACCTTCTTTCTAGCCCTTCAAAGATGCTGCCAGTGTTTCGCCCTAGAGTTATTACA
AAGCCAGTGCCAAAACCCAGCCATGGGCTCTTTGCAACCTCCCAGCTGCGCTCATTCAGCT
GACAGCGAGATGCAAGCAAAATGCTCAGCTCTCCTTACCCTGAAGGGGTCTCCCTGGAATGGA
AGTCCCCTGGCATGGTCAGTCCTCAGGCCCAAGACTCAAGTGTGCACAGACCCCTGTGTTCT
GCGGGTGAACAACTGCCCCACTAACCAGACTGGAAAACCCAGAAAGATGGGCCTTCCATGAAT
GCTTCATTCCAGAGGGACCAGAGGGCCTCCCTGTGCAAGGGATCAAGCATGTCTGGCCTGGG
TTTTCAAAAAAAGAGGGATCCTCATGACCTGGTGGTCTATGGCCTGGGTCAAGATGAGGGTC
TTTCAGTGTTCTGTTTACAACATGTCAAAGCCATTGGTTCAAGGGCGTAATAAATACTTGC
GTATTCAAAAA

FIGURE 48

MAVVSEDDFQHSSNSTYGTSSSLRADQEALLEKLLDRPPPGQLQRPEDRFCGTYYIFFSLGI
GSLLPWNFFITAKEYWMFKLRNSSSPATGEDPEGSDILNYFESYLAVASTVPSMLCLVANFL
LVNRVAVHIRVLASLTVILAIEMVITALVKVDTSSWTRGFFAVTIVCMVILSGASTVFSSSI
YGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSDVRNSALAFFLTATIFLVLCMGLY
LLLSRLEYARYYMRPVLAHVFSGEEELPQDSLAPSASRFIDSHTPPLRPILKKTASLGF
CVTYVFFITS LIYPAVCTNIESLNKSGSLWTTKFFIPLTTFLLYNFADLCGRQLTAWIQVP
GPNSKALPGFVLLRTCLIPLEVL CNYQPRVHLKTVVFQSDVYPALLSSLLGLSNGYLSTLAL
LYGPKIVPRELAEATGVVMSFYVCLGLTLGSACSTLLVHLI

Transmembrane domain:

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252,
305-330, 448-472

FIGURE 50

MAPLALHLLVLPILLSLVLASQDWKAERSQDPFEKCMQDPDYEQLLKVVVTWGLNRTLKPQRV
IVVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRI
HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPEKLGALRPQEKGHSPEDIYQMA
LNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMSDGGFFYLSFAEALR
AHSCLSDRLOYSRIVGGWDL LPRALLSSLSGLVLLNAPVVAMTQGPHDVHVQIETSPPARNL
KVLKADVLLTASGPAVKRITFSPPLPRHMQEALRRLHYVPATKVFLSFRPFWREEHIEGG
HSNTDRPSRMIFYPPPREGALLLASYTWSDAAAAFAGLSREEALRLALDDVAALHGPVVRQL
WDGTGVVKRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKS
ALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHGVASSPSHDLAKEEGSHPPVQGQLSLQ
NTTHTRTSH

Signal peptide:

amino acids 1-21

FIGURE 51

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAACTGGGGACACTCTGGGCCGGCCTTCTGCCTGCAT
GGACGCTCTGAAGCCACCCTGTCTCTGGAGGAACCACGAGCGAGGGAAGAAGGACAGGGACTCGTGTGGCAGGAA
 GAACTCAGAGCCGGGAAGCCCCCATTCACTAGAAGCACTGAGAGATGCGGCCCCCTCGCAGGGTCTGAATTTCT
 GCTGCTGTTACAAAGATGCTTTTTATCTTTAACTTTTTGTTTTCCCCACTTCCGACCCCGCGTGTGATCTGCAT
 CCTGACATTTGGAGCTGCCATCTTCTTGTGGCTGATCACCAGACCTCAACCCGTCTTACCTCTTCTTGACCTGAA
 CAATCAGTCTGTGGGAATTGAGGGAGGAGCACGGAAGGGGGTTTCCAGAGAAGAAATGACCTAACAAAGTTGCTG
 CTTCTCAGATGCCAAGACTATGTATGAGGTTTTCCAAAGAGGACTCGCTGTGTCTGACAATGGGCCCTGCTTGGG
 ATATAGAAAACCAAACCAGCCCTACAGATGGCTATCTTACAAACAGGTGTCTGATAGAGCAGAGTACCTGGGTTT
 CTGTCTCTTGACATAAAGGTTATAAATCATCACCAGACCAGTTTTGTGCGCATCTTTGCTCAGAATAGGCCAGAGTG
 GATCATCTCCGAATTGGCTTGTACACGTACTCTATGGTAGCTGTACCTCTGTATGACACCTTGGGACCAGAAGC
 CATCGTACATATTGTCAACAAGGCTGATATCGCCATGGTGTGATCTGTGACACACCCCAAAGGCATTGGTGCTGAT
 AGGGAATGTAGAGAAAGGCTTCAACCCGAGCCTGAAGGTGATCATCCTTATGGACCCCTTTGATGATGACCTGAA
 GCAAAGAGGGGAGAAGAGTGGAATTGAGATCTTATCCCTATATGATGCTGAGAACCTAGGCAAAGAGCACTTCAG
 AAAACCTGTGCCTCCTAGCCCAGAAGACCTGAGCGTCATCTGCTTACCAGTGGGACCACAGGTGACCCCAAAGG
 AGCCATGATAACCCATCAAAATATTGTTTTCAAATGCTGCTGCCCTTCTCAAATGTGTGGAGCATGCTTATGAGCC
 CACTCCTGATGATGTGGCCATATCCTACCTCCCTCTGGCTCATATGTTTGAGAGGATTGTACAGGCTGTTGTGTA
 CAGCTGTGGAGCCAGAGTTGGATTCTTCCAAGGGGATATTCGGTTGCTGGCTGACGACATGAAGACTTTGAAGCC
 CACATTGTTTTCCGCGGTGCCCTCGACTCCTTAACAGGATCTACGATAAGGTACAAAATGAGGCCAAGACACCCTT
 GAAGAAGTTCTTGTGAAGCTGGCTGTTTCCAGTAAATTCAAAGAGCTTCAAAGGGTATCATCAGGCATGATAG
 TTTCTGGGACAAGCTCATCTTTGCAAAGATCCAGGACAGCCTGGGCGGAAGGGTTCGTGTAATTGTCACTGGAGC
 TGCCCCCATGTCCACTTCAGTCATGACATTCTTCCGGGCAGCAATGGGATGTCAAGGTGTATGAAGCTTATGGTCA
 AACAGAATGCACAGGTGGCTGTACATTTACATTACCTGGGGACTGGACATCAGGTACAGTTGGGGTGCCCCCTGGC
 TTGCAATTACGTGAAGCTGGAAGATGTGGCTGACATGAACACTTTACAGTGAATAATGAAGGAGAGGTCTGCAT
 CAAGGGTACAAACGTGTTCAAAGGATACCTGAAGGACCTGAGAAGACACAGGAAGCCCTGGACAGTGATGGCTG
 GCTTCACACAGGAGACATTGGTCGCTGGCTCCCGAATGGAACCTCGAAGATCATCGACCGTAAAAAGAACATTTT
 CAAGCTGGCCCAAGGAGATACATTGCACCAGAGAAGATAGAAAATATCTACAACAGGAGTCAACCAGTGTTACA
 AATTTTTGTACACGGGGAGAGCTTACGGTCATCCTTAGTAGGAGTGGTGGTTCTTGACACAGATGTACTTCCCTC
 ATTTGCAGCCAAGCTTGGGGTGAAGGGCTCCTTTGAGGAACTGTGCCAAAACCAAGTTGTAAGGGAAGCCATTTT
 AGAAGACTTGCAGAAAATTGGGAAAGAAAGTGGCCTTAAACTTTTGAACAGGTCAAAGCCATTTTTCTTCATCC
 AGAGCCATTTTCCATTGAAAATGGGCTCTTGACACCAACATTGAAAGCAAAGCGAGGAGAGCTTTCCAAATACTT
 TCGGACCCAAATTGACAGCCTGTATGAGCACATCCAGGAT**TAG**GATAAGGTACTTAAGTACCTGCCGGCCCACTG
 TGCATGCTTGTGAGAAAATGGATTAAAACTATTCTTACATTTGTTTTGCCTTTCCTCCTATTTTTTTTTAACC
 TGTTAAACTCTAAAGCCATAGCTTTTGTTTTATATTGAGACATATAATGTGTAAACTTAGTTCCCAAATAAATCA
 ATCCTGTCTTTCCCATCTTCGATGTTGCTAATATTAAGGCTTCAGGGCTACTTTTATCAACATGCCTGTCTTCAA
 GATCCAGTTTATGTTCTGTGTCCTTCCTCATGATTTCCAACCTTAATACTATTAGTAACCACAAGTTCAAGGGT
 CAAAGGGACCCCTCTGTGCCTTCTTCTTTGTTTTGTGATAAACATAACTTGCCAACAGTCTCTATGCTTATTTACA
 TCTTCTACTGTTCAAACCTAAGAGATTTTAAATCTGAAAACTGCTTACAATTGATTTTTCTAGCCACTCCAC
 AAACCACTAAAATTTTAGTTTTAGCCTATCACTCATGTCAATCATATCTATGAGACAAATGTCTCCGATGCTCTT
 CTGCGTAAATTAAATTGTGTACTGAAGGGAAAAAGTTTATCATACCAAACATTTTCTAAACTCTCTAGTTAGATA
 TCTGACTTGGGAGTATTAAAAATTGGGTCTATGACATACTGTCCAAAAGGAATGCTGTTCTTAAAGCATTATTTA
 CAGTAGGAACCTGGGGAGTAAATCTGTTCCCTACAGTTTGTGCTGAGCTGGAAGCTGTGGGGGAAGGAGTTGACA
 GGTGGGCCCAAGTGAACTTTCCAGTAAATGAAGCAAGCACTGAATAAAAAACCTCCTGAACTGGGAACAAAGATCT
 ACAGGCAAGCAAGATGCCACACAACAGGCTTATTTTCTGTGAAGGAACCAACTGATCTCCCCACCCTTGGATT
 AGAGTTCCTGCTCTACCTTACCCACAGATAACACATGTTGTTTCTACTTGTAATGTAAAGTCTTTAAATAAAC
 TATTACAGATAAAAAA

FIGURE 52

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60775

<subunit 1 of 1, 739 aa, 1 stop

<MW: 82263, pI: 7.55, NX(S/T): 3

MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNLLLLFTKMLFIFN
 FLFSPLPTPALICILTFGAAIFLWLITRPQPVLPDLLNNSVGIEGGARKGVSQKNNDLTS
 CCFSDAKTMYEVFQRLAVSDNGPCLGYRKPNQPYRWLSYKQVSDRAEYLGSCLLHKGYKSS
 PDQFVGIFAQNRPEWIISELACYTYSMAVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQKAL
 VLIGNVEKGFTPSLKVIIILMDPFDDDLKQRGEKSGIEILSLYDAENLGKEHFRKPVPPSPED
 LSVICFTSGTTGDPKGAMITHQNIVSNAAAFLKCVEHAYEPTPDDVAISYLPLAHMFERIVQ
 AVVYSCGARVGGFFQGDIRLLADDMKTLKPTLFPAPVPRLLNRIYDKVQNEAKTPLKKFLLKLA
 VSSKFELQKGIIRHDSFWDKLIFAKIQDSLGRVRVIVTGAAPMSTSVMTFFRAAMGCQVY
 EAYGQTECTGGCTFTLPGDWTSGHVGVPACNYVKLEDVADMNYFTVNNEGEVCIKGTNVFK
 GYLKDPEKTQEALDSGWLHTGDIGRWLPNGTLKIIDRKKNIKLAQGEYIAPEKIENIYNR
 SQPVLQIFVHGESLRSSLVGVVVPDPTDVLPSFAAKLGVKGSFEELCQNQVVREAILEDLQKI
 GKESGLKTFEQVKAIFLHPEPFSIENGLLTPTLKAKRGELSKYFRTQIDSLYEHIQD

Important features:

Type II transmembrane domain:

amino acids 61-80

Putative AMP-binding domain signature.

amino acids 314-325

N-glycosylation site.

amino acids 102-105, 588-591 and 619-622

FIGURE 53

GGAGGCGGAGGCCGCGGCGAGCCGGGCGAGCAGTGAGGGCCCTAGCGGGGCCCCGAGCGGGG
 CCCGGGGCCCCCTAAGCCATTCTGAAGTCATGGGCTGGCCAGGACATTGGTGACCCGCCAAT
 CCGGT**ATG**GACGACTGGAAGCCCAGCCCCCTCATCAAGCCCTTGGGGCTCGGAAGAAGCGG
 AGCTGGTACCTTACCTGGAAGTATAAACTGACAAACCAGCGGGCCCTGCGGAGATTCTGTCA
 GACAGGGGGCCGTGCTTTTCTGCTGGTGAAGTGTCAATTGTCAATATCAAGTTGATCCTGGACA
 CTCGGCGAGCCATCAGTGAAGCCAATGAAGACCCAGAGCCAGAGCAAGACTATGATGAGGCC
 CTAGGCCGCTGGAGCCCCCACGGCGCAGAGGCAGTGGTCCCCGGCGGGTCTGGACGTAGA
 GGTGTATTCAAGTCGCAGCAAAGTATATGTGGCAGTGGATGGCACCACGGTGCTGGAGGATG
 AGGCCCGGGAGCAGGGCCGGGGCATCCATGTCATTGTCTCAACCAGGCCACGGGCCACGTG
 ATGGCAAAACGTGTGTTTGACACGTACTCACCTCATGAGGATGAGGCCATGGTGCTATTCT
 CAACATGGTAGCGCCCCGGCCGAGTGCTCATCTGCACTGTCAAGGATGAGGGCTCCTTCCACC
 TCAAGGACACAGCCAAGGCTCTGCTGAGGAGCCTGGGCAGCCAGGCTGGCCCTGCCCTGGGC
 TGGAGGGACACATGGGCCTTCGTGGGACGAAAAGGAGGTCTGTCTTCGGGGAGAAACATTC
 TAAGTCACCTGCCCTCTCTTCTGGGGGGACCCAGTCTGCTGAAGACAGATGTGCCATTGA
 GCTCAGCAGAAGAGGCAGAGTGCCACTGGGCAGACACAGAGCTGAACCGTCGCCGCCGGCGC
 TTCTGCAGCAAAGTTGAGGGCTATGGAAGTGTATGCAGCTGCAAGGACCCACACCCATCGA
 GTTCAGCCCTGACCCACTCCAGACAACAAGGTCTCAATGTGCCTGTGGCTGTCATTGCAG
 GGAACCGACCCAATTACCTGTACAGGATGCTGCGCTCTCTGCTTTCAGCCAGGGGGTGTCT
 CCTCAGATGATAACAGTTTTTCATTGACGGCTACTATGAGGAACCCATGGATGTGGTGGCACT
 GTTTGGTCTGAGGGGCATCCAGCATACTCCCATCAGCATCAAGAATGCCCGCGTGTCTCAGC
 ACTACAAGGCCAGCCTCACTGCCACTTTCAACCTGTTTCCGGAGGCCAAGTTTGTGTGGTT
 CTGGAAGAGGACCTGGACATTGCTGTGGATTTTTTTCAGTTTCTGAGCCAATCCATCCACCT
 ACTGGAGGAGGATGACAGCCTGTACTGCATCTCTGCCTGGAATGACCAGGGGTATGAACACA
 CGGCTGAGGACCCAGCACTACTGTACCGTGTGGAGACCATGCCTGGGCTGGGCTGGGTGCTC
 AGGAGGTCTTGTACAAGGAGGAGCTTGAGCCCCAAGTGGCCTACACCGGAAAAGCTCTGGGA
 TTGGGACATGTGGATGCGGATGCCTGAACAACGCCGGGGCCGAGAGTGCATCATCCCTGACG
 TTTCCCGATCCTACCACTTTGGCATCGTCGGCCTCAACATGAATGGCTACTTTACAGAGGCC
 TACTTCAAGAAGCACAAAGTTCAACACGGTTCCAGGTGTCCAGCTCAGGAATGTGGACAGTCT
 GAAGAAAGAAGCTTATGAAGTGAAGTTTACAGGCTGCTCAGTGAGGCTGAGGTTCTGGACC
 ACAGCAAGAACCCTTGTGAAGACTCTTCTCTGCCAGACACAGAGGGCCACACCTACGTGGCC
 TTTATTCGAATGGAGAAAGATGATGACTTCACCACCTGGACCCAGCTTGCCAAGTGCCTCCA
 TATCTGGGACCTGGATGTGCGTGGCAACCATCGGGGCTGTGGAGATTGTTTCGGAAGAAGA
 ACCACTTCCTGGTGGTGGGGGTCCCCGCTTCCCCCTACTCAGTGAAGAAGCCACCCTCAGTC
 ACCCCAATTTTCTGGAGCCACCCCCAAAGGAGGAGGGAGCCCCAGGAGCCCCAGAACAGAC
ATGAGACCTCCTCCAGGACCCTGCGGGGCTGGGTACTGTGTACCCCCAGGCTGGCTAGCCCT
 TCCCTCCATCCTGTAGGATTTTGTAGATGCTGGTAGGGGCTGGGGCTACCTTGTTTTTAACA
 TGAGACTTAATTACTAACTCCAAGGGGAGGGTTCCCTGCTCCAACACCCCGTTCTGAGTT
 AAAAGTCTATTTATTTACTTCTTGTGGAGAAGGGCAGGAGAGTACCTGGGAATCATTACG
 ATCCCTAGCAGCTCATCCTGCCCTTTGAATACCCTCACTTTCCAGGCCTGGCTCAGAATCTA
 ACCTATTTATTGACTGTCTGAGGGCCTTGAAAACAGGCCGAACCTGGAGGGCCTGGATTTT
 TTTTGGGCTGGAATGCTGCCCTGAGGGTGGGGCTGGCTCTTACTCAGGAACTGCTGTGCC
 CAACCCATGGACAGGCCAGCTGGGGCCCATGCTGACACAGACTCACTCAGAGACCCTTA
 GACTGAGACCAGGCCTCCTCTCAGCCTTCTCTTTGTCCAGATTTCCAAAGCTGGATAAGTT
 GGTCAATTGATTAAAAAAGGAGAAGCCCTCTGGGAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 54

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA61185

><subunit 1 of 1, 660 aa, 1 stop

><MW: 75220, pI: 6.76, NX(S/T): 0

MDDWKPSPLIKPFGARKKRSWYLTWKYKLTNQALRRFCQTGAVLFLLVTIVNIKLILDTR
RAISEANEDPEPEQDYDEALGRLEPPRRRGSGPRRVLDVEVYSSRSKVYVAVDGTTVLEDEA
REQGRGIHVIVLNQATGHVMAKRVFDTYSPHEDEAMVLFNLMVAPGRVLICTVKDEGSFHLK
DTAKALLRSLGSQAGPALGWRDWFVGRKGGPVFGEKHSKSPALSSWGDPVLLKTDVPLSS
AEEAECHWADTELNRRRRRFCSKVEGYGSCSKDPTPIEFSPDPLPDNKVLNVPVAVIAGN
RPNYLYRMLRSLLSAQGVSPQMITVFIDGYEPEMDVVALFGLRGIQHTPISIKNARVSQHY
KASLTATFNLFPFAKFAVVLEEDLDIAVDFFSFLSQSIHLLEEDDSLYCISAWNDQGYEHTA
EDPALLYRVETMPGLGWVLRRLSYKEELEPKWPTPEKLWDWDMWMMRMPEQRRGRECIIPDVS
RSYHFGIVGLNMNGYFHEAYFKKHKFNTVPGVQLRNVDLSLKKEAYEVEVHRLLSAEVLDHS
KNPCEDSFLPDTEGHTYVAFIRMEKDDDFTTWTQLAKCLHIWDLDVGRGNHRGLWRLFRKKNH
FLVVGVPASPYSVKKPPSVTPIFLEPPPKEEGAPGAPEQT

Important features of the protein:**Transmembrane domain:**

amino acids 38-55

Homologous region to Mouse GNT1

amino acids 229-660

FIGURE 55

CGGACGCGTGGGCTGCTGGTGGGAAGGCCTAAAGAACTGGAAAGCCCACTCTCTTGGAAACCACCACAC
 CTGTTTAAAGAACCTAAGCACCATTTAAAGCCCACTGGAAATTTGTTGTCTAGTGGTTGTGGGTGAATA
 AAGGAGGGCAGAAATGATGATTTTCATCTCCATTAGCCTGCTGTCTCTGGCTATGTTGGTGGGATGTTA
 CGTGGCCGGAATCATTCCCTTGGCTGTTAATTTCTCAGAGGAACGACTGAAGCTGGTGAAGTGTGTTTGG
 GTGCTGGCCTTCTCTGTGGAAGTGTCTGGCAGTCATCGTGCCTGAAGGAGTACATGCCCTTTATGAA
 GATATTTCTGAGGGAAAACACCACCAAGCAAGTGAAACACATAATGTGATTGCATCAGACAAAGCAGC
 AGAAAAATCAGTTGTCCATGAACATGAGCACAGCCACGACCACACACAGCTGCATGCCCTATATTGGTG
 TTTCCCTCGTTCTGGGCTTCGTTTTTCATGTTGCTGGTGGACCAGATTGGTAACCTCCATGTGCATTCT
 ACTGACGATCCAGAAGCAGCAAGGTCTAGCAATTTCCAAAATCACCACCACGCTGGGTCTGGTTGTCCA
 TGCTGCAGCTGATGGTGTGCTTTTGGGAGCAGCAGCATCTACTTCACAGACCAGTGTCCAGTTAATTG
 TGTTTGTGGCAATCATGCTACATAAGGCACCAGCTGCTTTTGGACTGGTTTCCTTCTTGATGCATGCT
 GGCTTAGAGCGGAATCGAATCAGAAAGCACTTGTGGTCTTTGCATTGGCAGCACCAGTTATGTCCAT
 GGTGACATACTTAGGACTGAGTAAGAGCAGTAAAGAAGCCCTTTTCCAGAGGTGAACGCCACGGGAGTGG
 CCATGCTTTTCTCTGCCGGGACATTTCTTTATGTTGCCACAGTACATGTCTCCCTGAGGTGGGCGGA
 ATAGGGCACAGCCACAAGCCCGATGCCACGGGAGGGAGAGGCCTCAGCCGCCTGGAAGTGGCAGCCCT
 GGTTCTGGGTTGCCTCATCCCTCTCATCCTGTCTAGTAGGACACCAGCATTAATGTTCAAGGTCCAGC
 CTTGGTCCAGGGCCGTTTGGCCATCCAGTGAGAACAGCCGGCACGTGACAGCTACTCACTTCCTCAGTC
 TCTTGTCTCACCTTGGCAGTCTCTACATGTATTCCTAGAGTCCAGAGGGGAGGTGAGGTTAAACCTG
 AGTAATGGAAAAGCTTTTAGAGTAGAAACACATTTACGTTGCAGTTAGCTATAGACATCCCATTTGTGT
 TATCTTTTAAAGGCCCTTGACATTTTGCCTTTAATATTTCTCTTAACCCTATTCTCAGGGAAGATG
 GAATTTAGTATTTAAGGAAAAGAGGAGAACTTCATACTCACAATGAAATAGTGATTATGAAAATACAGT
 GTTCTGTAATTAAGCTATGTCTCTTTCTTCTAGTTTAGAGGCTCTGCTACTTTATCCATTGATTTTT
 AACATGGTTCCCACCATGTAAGACTGGTGCTTTAGCATCTATGCCACATGCGTTGATGGAAGGTCATA
 GCACCCACTCACTTAGATGCTAAAGGTGATTCTAGTTAATCTGGGATTAGGGTCAGGAAAATGATAGC
 AAGACACATTGAAAGCTCTCTTTATACTCAAAGAGATATCCATTGAAAAGGGATGTCTAGAGGGATT
 TAAACAGCTCCTTTGGCACGTGCCTCTCTGAATCCAGCCTGCCATTCCATCAAATGGAGCAGGAGAGG
 TGGGAGGAGCTTCTAAAGAGGTGACTGGTATTTTGTAGCATTCCTTGTCAAGTTCTCCTTTGCAGAAT
 ACCTGTCTCCACATTCCCTAGAGAGGAGCCAAGTTCTAGTAGTTTCAGTTCTAGGCTTTCTCCTCAAGAA
 CAGTCAGATCACAAAGTGCTTTTGGAAATTAAGGGATATTAATTTTAAAGTGATTTTTGGATGGTTAT
 TGATATCTTTGTAGTAGCTTTTTTTTAAAGACTACCAAAATGTATGGTTGTCCTTTTTTTTTGTTTTT
 TTTTTTTTTAATTATTTCTCTTAGCAGATCAGCAATCCCTCTAGGGACCTAAATACTAGGTGAGCTTT
 GGCGACACTGTGTCTTCTCACATAACCACCTGTAGCAAGATGGATCATAAATGAGAAGTGTTTGCCTA
 TTGATTTAAAGCTTATTGGAATCATGTCTCTTGTCTCTTCTGCTTTTCTTTGCTTTTCTTCTAACTTT
 TCCCTCTAGCCTCTCCTCGCCACAATTTGCTGCTTACTGCTGGTGTGTTAATATTGTGTGGGATGAATT
 CTTATCAGGACAACCACCTTCTCGAAGTGAATAATGAAGATAATAATATCTTTATCTTTATCCCTT
 CAAAGAAATTACCTTTGTGTCAAATGCCGCTTTGTTGAGCCCTTAAATAACCACCTCCTCATGTGTAA
 ATTGACACAATCACTAATCTGGTAATTTAAACAATTGAGATAGCAAAAGTGTTTAAACAGACTAGGATA
 ATTTTTTTTTTCATATTTGCCAAAATTTTGTAAACCCTGTCTGTCAAATAAGTGTTAATATTGTAT
 TATTAATTTATTTTACTTTCTATACCATTTCAAACACATTACACTAAGGGGGAACCAAGACTAGTT
 TCTTCAGGGCAGTGGACGTAGTAGTTTGTAAAAACGTTTTCTATGACGCATAAGCTAGCATGCCTATG
 ATTTATTTTCTTCATGAATTTGTCACTGGATCAGCAGCTGTGGAATAAAGCTTGTGAGCCCTCTGCT
 GGCCACAGTGAGGAAAGTAGCACAAATAGGATACAGTTGTATGTAGTCATTGGCAACAATTGCATACA
 ATTTTACTACCAAGAGAAGGTATAGTATGGAAAGTCCAAATGACTTCCTTGATTGGATGTTAACAGCT
 GACTGGTGTGAGACTTGAGGTTTCATCTAGTCCTTCAAACCTATATGGTTGCCTAGATTCTCTCTGGA
 AACTGACTTTGTCAAATAAATAGCAGATTGTAGTGTCAAAAAA

FIGURE 56

MDDFISISLLSLAMLVGCVAGIIP LAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHAL
YEDILEGKHHQASETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVFMLLVDQ
IGNSHVHSTDDPEAARSSNSKITTTLGLVVHAAADGVALGAAASTSQT SVQLIVFVAIMLHK
APAAFGLVSFLMHAGLERNRIRKHL LVFALAAPVMSMVTYLGLSKSSKEALSEVNATGVAML
FSAGTFLYVATVHVLPEVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIP LILSVGHQH

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 37-56, 106-122, 211-230, 240-260, 288-304

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FIGURE 58

MMGLGNRRSMKSPPLVLAALVACIIIVLGFNYWIIASSRSVDLQTRIMELEGRVRRAAAERGA
VELKKNEFQGELEKQREQLDKIQSSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQL
KTLQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVA
SRDLSENNDQRQQLOALSEPQPRQLQAAGLPHTTEVPQGKGNVLGNSKSQTPAPSSEVVLDSCR
QVEKEETNEIQVVNEEPQORDRLPQEPGREQVVEDRPVGGRGFGGAGELGQTPQVQAALSVSQ
ENPEMEGPERDQLVIPDGQEEEQEAAGEGRNQQLRGEDDYNMDENEAESETDKQAALAGND
RNIDVFNVEDQKRDTINLLDQREKRNHTL

Signal peptide:

amino acids 1-29

FIGURE 59

GGATGCAGAAAGCCTCAGTGTTGCTCTTCCCTGGCCTGGGTCTGCTTCCCTCTTCTACGCTGGCATTGCCCTCTTCA
 CCAGTGGCTTCCTGCTCACCCGTTTGGAGCTCACCAACCATAGCAGCTGCCAAGAGCCCCAGGCCCTGGGTCCC
 TGCCATGGGGGAGCCAAGGGAAACCTGGGGCCTGCTGGATGGCTTCCCGATTTTCGCGGGTTGTGTTGGTGCTGA
 TAGATGCTCTGCGATTTGACTTCGCCCAGCCCCAGCATTACACAGTGCCTAGAGAGCCTCCTGTCTCCCTACCCT
 TCCTGGGCAAACCTAAGCTCCTTGACAGAGGATCCTGGAGATTACAGCCCCACCATGCCCGGCTCTACCGATCTCAGG
 TTGACCCTCCTACCACCACCATGCAGCGCCTCAAGGCCCTCACCAGTGGCTCACTGCCTACCTTTATTGATGCTG
 GTAGTAACCTCGCCAGCCACGCCATAGTGGAGACAATCTCATTAAAGCAGCTCACCAGTGCAGGAAGGCGTGAG
 TCTTCATGGGAGATGATACCTGGAAAGACCTTTTCCCTGGTGCTTTCTCCAAAGCTTTCTTCTTCCCATCCTTCA
 ATGTCAGAGACCTAGACACAGTGGACAATGGCATCCTGGAAACACCTCTACCCACCATGGACAGTGGTGAATGGG
 ACGTGCTGATTGCTCACTTCCTGGGTGTGGACCACTGTGGCCACAAGCATGGCCCTCACCACCCTGAAATGGCCA
 AGAAACTTAGCCAGATGGACCAGGTGATCCAGGGACTTGTGGAGCGTCTGGAGAATGACACACTGCTGGTAGTGG
 CTGGGGACCATGGGATGACCACAAATGGAGACCATGGAGGGGACAGTGAGCTGGAGGTCTCAGCTGCTCTCTTTC
 TGTATAGCCCCACAGCAGTCTTCCCCAGCACCCACAGAGGAGCCAGAGGTGATTCTCAAGTTAGCCTTGTGC
 CCACGCTGGCCCTGCTGCTGGGCCCTGCCATCCCATTTGGGAATATCGGGGAAGTGATGGCTGAGCTATTCTCAG
 GGGGTGAGGACTCCCAGCCCCACTCCTCTGCTTTAGCCCCAAGCCTCAGCTCTCCATCTCAATGCTCAGCAGGTGT
 CCCGATTTCTTCATACCTACTCAGCTGCTACTCAGGACCTTCAAGCTAAGGAGCTTCATCAGCTGCAGAACCTCT
 TCTCCAAGGCCTCTGCTGACTACCAGTGGCTTCTCCAGAGCCCCAAGGGGGCTGAGGCGACACTGCCGACTGTGA
 TTGCTGAGCTGCAGCAGTTCCTGCGGGGAGCTCGGGCCATGTGCATCGAGTCTTGGGCTCGTTTTCTCTCTGGTCC
 GCATGGCGGGGGGTACTGCTCTCTTGGCTGCTTCTGCTTTATCTGCCTGCTGGCATCTCAGTGGGCAATATCCC
 CAGGCTTTCCATTCTGCCCTCTACTCCTGACACCTGTGGCCTGGGGCCTGTTGGGGCCATAGCGTATGCTGGAC
 TCCTGGGAACCTATTGAGCTGAAGCTAGATCTAGTGCTTCTAGGGGCTGTGGCTGCAGTGAGCTCATTCCCTCCCTT
 TTCTGTGGAAAGCCTGGGCTGGCTGGGGGTCCAAGAGGCCCCCTGGCAACCCTGTTTCCCATCCCTGGGCCCCGTC
 TGTTACTCCTGCTGTTTTGCTTGGCTGTGTTCTCTCTGATAGTTTTGTTGTAGCTGAGGCCAGGGCCACCCCT
 TCCTTTTGGGCTCATTATCCTGCTCCTGCTTGTCCAGCTTCACTGGGAGGGCCAGCTGCTTCCACCTAAGCTAC
 TCACAATGCCCCGCCTTGGCACTTCAGCCACAACAAACCCCCACGGGCACAATGGTGCATATGCCCTGAGGCTTG
 GAATTGGGTTGCTTTTATGTACAAGGCTAGCTGGGCTTTTTCATCGTTGCCCTGAAGAGACACCTGTTTGGCACT
 CCTCTCCCTGGCTGAGTCCCTTGGCATCCATGGTGGGTGGTTCGAGCCAAGAATTTATGGTATGGAGCTTGTGTGG
 CGGCGCTGGTGGCCCTGTTAGCTGCCGTGCGCTTGTGGCTTCGCGCTATGGTAATCTCAAGAGCCCCGAGCCAC
 CCATGCTCTTTGTGCGCTGGGACTGCCCTAATGGCATTGGGTACTGCTGCCTACTGGGCATTGGCGTGGGGG
 CAGATGAGGCTCCCCCGCTCTCCGGTCTGGTCTCTGGGGCATCCATGGTGTGCTCGGGCTGTAGCAGGGC
 TGGCTGCTTCAGGGCTCGCGCTGCTGCTCTGGAAGCCTGTGACAGTGTGGTGAAGGCTGGGGCAGGCGCTCCAA
 GGACCAGGACTGTCTCACTCCCTTCTCAGGCCCCCCCCACTTCTCAAGCTGACTTGGATTATGTGGTCCCTCAAA
 TCTACCGACACATGCAGGAGGAGTTCCGGGGCCGGTTAGAGAGGACCAATCTCAGGGTCCCCTGACTGTGGCTG
 CTTATCAGTTGGGGAGTGTCTACTCAGCTGCTATGGTCACAGCCCTCACCTGTTGGCCTTCCCCTTCTGCTGT
 TGCATGCGGAGCGCATCAGCCTTGTGTTCTGCTTCTGTTTCTGCAGAGCTTCTTCTCTACATCTGCTTGCTG
 CTGGGATACCCGTACCACCCCTGGTCTTTTACTGTGCCATGGCAGGCAGTCTCGGCTTGGGCCCTCATGGCCA
 CACAGACCTTCTACTCCACAGGCCACCAGCCTGTCTTCCAGCCATCCATTGGCATGCAGCCTTTCGTGGGATTCC
 CAGAGGGTCATGGCTCCTGTACTTGGCTGCCTGCTTTGCTAGTGGGAGCCAACACCTTTGCCTCCCACCTCCTCT
 TTGCAGTAGGTTGCCCACTGCTCCTGCTCTGGCCTTTTCTGTGTGAGAGTCAAGGGCTGCGGAAGAGACAGCAGC
 CCCCAGGGAATGAAGCTGATGCCAGAGTCAGACCCGAGGAGGAAGAGGAGCCACTGATGGAGATGCGGCTCCGGG
 ATGCGCCTCAGCACTTCTATGCAGCACTGCTGCAGCTGGGCTCAAGTACCTCTTTATCCTTGGTATTTCAGATTC
 TGGCCTGTGCCCTTGGCAGCCTCCATCCTTCGAGGCATCTCATGGTCTGGAAAGTGTGTTGCCCTAAGTTTCATAT
 TTGAGGCTGTGGGCTTCATTGTGAGCAGCGTGGGACTTCTCCTGGGCATAGCTTTGGTGATGAGAGTGGATGGTG
 CTGTGAGCTCCTGGTTCAGGCAGCTATTTCTGGCCCCAGCAGAGG**TAG**CCTAGTCTGTGATTACTGGCACTTGGCT
 ACAGAGAGTGTGGAGAACAGTGTAGCCTGGCCTGTACAGGTACTGGATGATCTGCAAGACAGGCTCAGCCATAC
 TCTTACTATCATGCAGCCAGGGGCCGCTGACATCTAGGACTTCATTATTCTATAATTACAGGACCACAGTGGAGTA
 TGATCCCTAACTCCTGATTTGGATGCATCTGAGGGACAAGGGGGGCGGTCTCCGAAGTGGAATAAAATAGGCCGG
 GCGTGGTGACTTGCACCTATAATCCCAGCACTTTGGGAGGCAGAGGTGGGAGGATTGCTTGGTCCCAGGAGTTCA
 AGACCAGCCTGTGGAACATAACAAGACCCCGTCTCTACTATTTAAAAAAAAGTGAATAAAATGATAATAT

FIGURE 60

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809

<subunit 1 of 1, 1089 aa, 1 stop

<MW: 118699, pI: 8.49, NX(S/T): 2

MQKASVLLFLAWVCFLFYAGIALFTSGFLLTRLELTNHSSCQEPPGPGSLPWGSQGKPGACW
 MASRFSRVVLVLIDALRFDFQAQPQHSHVPREPPVSLPFLGKLSSLQRILEIQPHHARLYRSQ
 VDPPTTTMQRLKALTGSLPTFIDAGSNFASHAIVEDNLIKQLTSAGRRVVFMGDDTWKDLF
 PGAFSKAFFFPSFNVRDLDTVDNGILEHLYPTMDSGEWDVLIAHFLGVDHCGHKHGPHPHP
 AKKLSQMDQVIQGLVERLENDTLLVVAGDHGMTTNGDHGGDSELEVSAALFLYSPTAVFPST
 PPEEPEVIPQVSLVPTLALLLGLPIPFNGI GEVMAELFSGGEDSQPHSSALAQASALHLNAQ
 QVSRFLHTYSAATQDLQAKELHQLQNLFSKASADYQWLLQSPKGAEATLPTVIAELQQFLRG
 ARAMCIESWARFSLVRMAGGTALLAASCFCILLASQWAISPGFPFCPLLLTPVAWGLVGAIA
 YAGLLGTIELKLDLVLLGAVAAVSSFLPFLWKAWAGWGSKRPLATLFPPIPGPVLLLLLLFRLA
 VFFSDSFVVAEARATPFLGSEFILLVVLVQLHWEGQLLPKLLTMPRLGTSATTNPPRHNGAY
 ALRLGIGLLLCTRLAGLFHRCPEETPVCHSSPWLSPLASMVGGRAKNLWYGACVAALVALLA
 AVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPPRLRVLVSGASMVL
 RAVAGLAASGLALLLWKPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYRHMQE
 EFRGRLERTKSQGPLTVAAAYQLGSVYSAAMVTALTLLAFPLLLLHAERISLVFLLLFLQSFL
 LLHLLAAGIPVTTGPFPTVPWQAVSAWALMATQTFYSTGHQPVPFPAIHWHAFAVGFPEGHGS
 CTWLPALLVGANTFASHLLFAVGCPLLLLWPFLLCESQGLRKRQQPPGNEADARVRPEEEEEEP
 LMEMRLRDAPQHFYAALLQLGLKYLFI LGIQLACALAASILRRHLMVWKVFAPKFIFEAVG
 FIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQQR

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domains:

amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850,
 1016-1034, 1052-1070

Leucine zipper pattern.

amino acids 843-864

N-glycosylation sites.

amino acids 37-40, 268-271

FIGURE 62

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815

<subunit 1 of 1, 442 aa, 1 stop

<MW: 49932, pI: 4.55, NX(S/T): 5

MSYNGLHQRVFKELKLLTLCSSISQIGPPEVALTTDEKSISSVVLTAPEKWKRNPEDLPVSMQ
QIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRRAQPSEKQ
CARTLKDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILYIGNEFD
KRFFVPAEKIVINFITLNISSDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKH
LGYASHLMEIFCDSEENTEGTSLTQQESLSRTIPDKTVIEYEYDVRTTDICAGPEEQELSL
QEEVSTQGTLLESQAALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEEPSTTLVDWD
PQTGRLCIPSLSSFDQDSEGCEPSEGDLGEEGLLSRLYEPPAPDRPPGENETYLMQFMEEW
GLYVQMEN

Important features:**Signal peptide:**

amino acids 1-28

Transmembrane domain:

amino acids 140-163

N-glycosylation sites.

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

FIGURE 63

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTCTCTGCGGGGAGACGCCAGCCTGCG
TCTGCC**ATG**GGGCTCGGGTTGAGGGGCTGGGGACGTCTCTGCTGACTGTGGCCACCGCCCT
GATGCTGCCCCTGAAGCCCCCGCAGGCTCCTGGGGGGGCCAGATCATCGGGGGCCACGAGG
TGACCCCCCACTCCAGGCCCTACATGGCATCCGTGCGCTTCGGGGGCCAACATCACTGCGGA
GGCTTCCTGCTGCGAGCCCGCTGGGTGGTCTCGGCCGCCCACTGCTTCAGCCACAGAGACCT
CCGCACTGGCCTGGTGGTGGTGGGCGCCACGTCTGAGTACTGCGGAGCCCAACCAGCAGG
TGTTTGGCATCGATGCTCTCACCACGCACCCCGACTACCACCCCATGACCCACGCCAACGAC
ATCTGCCTGCTGCGGCTGAACGGCTCTGCTGTCTGGGCCCTGCAGTGGGGCTGCTGAGGCT
GCCAGGGAGAAGGGCCAGGCCCCCACAGCGGGGACACGGTGCCGGGTGGCTGGCTGGGGCT
TCGTGTCTGACTTTGAGGAGCTGCCGCCTGGACTGATGGAGGCCAAGGTCCGAGTGCTGGAC
CCGGACGTCTGCAACAGCTCCTGGAAGGGCCACCTGACACTTACCATGCTCTGCACCCGCAG
TGGGGACAGCCACAGACGGGGCTTCTGCTCGGCCGACTCCGGAGGGGCCCTGGTGTGCAGGA
ACCGGGCTCACGGCCTCGTTTCCTTCTCGGGCCTCTGGTGCGGCGACCCCAAGACCCCGAC
GTGTACACGCAGGTGTCCGCCTTTGTGGCCTGGATCTGGGACGTGGTTCGGCGGAGCAGTCC
CCAGCCCGGCCCCCTGCCTGGGACCACCAGGCCCCCAGGAGAAGCCGCC**TGA**GCCACAACCT
TGCGGCATGCAAATGAGATGGCCGCTCCAGGCCTGGAATGTTCCGTGGCTGGGCCCCACGGG
AAGCCTGATGTTTCAGGGTTGGGGTGGGACGGGCAGCGGTGGGGCACACCCATTCCACATGCA
AAGGGCAGAAGCAAACCCAGTAAATGTAACTGACAAAAAAAAAAAAAAAAAAAAAGAAA

FIGURE 66

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842

><subunit 1 of 1, 331 aa, 1 stop

><MW: 35932, pI: 8.45, NX(S/T): 1

MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARRG
GNIILACRDMEKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIEEEERV DILINN
AGVMRCPHWTTEDGFEMQFGVNHLGHFLLTNLLLDK LKASAPSRIINLSSLAHVAGHIDFDD
LNWQTRKYNTKAAYCQSKLAIVLFTKELSRRLQSGSVTVNALHPGVARTELGRHTGIHGSTF
SSTTLGPIFWLLVKSPELAAQPSTYLAVAEELADVSGKYFDGLKQKAPAPEAEDEEVARRLW
AESARLVGLEAPSVREQPLPR

Signal peptide:

amino acids 1-17

66/249

FIGURE 67

GAAGTTTCGCGAGCGCTGGC**ATGT**GGTCTCTGGGGCGCGGCTGGCGGCGCTGCTGGCGGTGCTG
GCGCTCGGGACAGGAGACCCAGAAAGGGCTGCGGCTCGGGGCGACACGTTCTCGGCGCTGAC
CAGCGTGGCGCGCGCCCTGGCGCCCGAGCGCCGGCTGCTGGGGCTGCTGAGGCGGTACCTGC
GCGGGGAGGAGGCGCGGCTGCGGGACCTGACTAGATTCTACGACAAGGTACTTTCTTTGCAT
GAGGATTCAACAACCCCTGTGGCTAACCCCTCTGCTTGCAATTTACTCTCATCAAACGCCTGCA
GTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGG
ATGGCTATGAGAAAGGTGGAGCAAGACCTTCCAGCCTTTGAGGACCTTGAGGGAGCAGCAAGG
GCCCTGATGCGGCTGCAGGACGTGTACATGCTCAATGTGAAAGGCCTGGCCCGAGGTGTCTT
TCAGAGAGTCACTGGCTCTGCCATCACTGACCTGTACAGCCCCAAACGGCTCTTTTCTCTCA
CAGGGGATGACTGCTTCCAAGTTGGCAAGGTGGCCTATGACATGGGGGATTATTACCATGCC
ATTCCATGGCTGGAGGAGGCTGTCACTCTCTTCCGAGGATCTTACGGAGAGTGGAAAGACAGA
GGATGAGGCAAGTCTAGAAGATGCCTTGGATCACTTGGCCTTTGCTTATTTCCGGGCGAGGAA
ATGTTTCGTGTGCCCTCAGCCTCTCTCGGGAGTTTCTTCTCTACAGCCCAGATAATAAGAGG
ATGGCCAGGAATGTCTTGAAATATGAAAGGCTCTTGGCAGAGAGCCCCAACCACGTGGTAGC
TGAGGCTGTCATCCAGAGGCCCAATATACCCACCTGCAGACCAGAGACACCTACGAGGGGC
TATGTCAGACCCTGGGTTCCAGCCCACTCTCTACCAGATCCCTAGCCTCTACTGTTCCCTAT
GAGACCAATTCCAACGCCTACCTGCTGCTCCAGCCCATCCGGAAGGAGGTGATCCACCTGGA
GCCCTACATTGCTCTCTACCATGACTTCGTCACTGACTCAGAGGCTCAGAAAATTAGAGAAC
TTGCAGAAACCATGGCTACAGAGGTCAGTGGTGGCATCAGGGGAGAAGCAGTTACAAGTGGAG
TACCGCATCAGCAAAAGTGCCTGGCTGAAGGACACTGTTGACCCAAAACCTGGTGACCCTCAA
CCACCGCATTTGCTGCCCTCACAGGCCTTGATGTCCGGCCTCCCTATGCAGAGTATCTGCAGG
TGGTGAACCTATGGCATCGGAGGACACTATGAGCCTCACTTTGACCATGCTACGTACCAAGC
AGCCCCCTCTACAGAATGAAGTCAGGAAACCGAGTTGCAACATTTATGATCTATCTGAGCTC
GGTGGAAAGCTGGAGGAGCCACAGCCTTCATCTATGCCAACCTCAGCGTGCCTGTGGTTAGGA
ATGCAGCACTGTTTTGGTGGAAACCTGCACAGGAGTGGTGAAGGGGACAGTGACACACTTCAT
GCTGGCTGTCCTGTCCTGGTGGGAGATAAGTGGGTGGCCAACAAGTGATACATGAGTATGG
ACAGGAATTCCGCAGACCCTGCAGCTCCAGCCCTGAAGAC**TGA**ACTGTTGGCAGAGAGAAGC
TGGTGGAGTCTGTGGCTTTCCAGAGAAGCCAGGAGCCAAAGCTGGGGTAGGAGAGGAGAA
AGCAGAGCAGCCTCCTGGAAGAAGGCCTTGTCAGCTTTGTCTGTGCCTCGCAAATCAGAGGC
AAGGGAGAGGTTGTTACCAGGGGACACTGAGAATGTACATTTGATCTGCCCCAGCCACGGAA
GTCAGAGTAGGATGCACAGTACAAAGGAGGGGGGAGTGGAGGCCTGAGAGGGGAAGTTTCTGG
AGTTCAGATACTCTCTGTTGGGAACAGGACATCTCAACAGTCTCAGGTTGATCAGTGGGTC
TTTTGGCACTTTGAACCTTGACCACAGGGACCAAGAAGTGGCAATGAGGACACCTGCAGGAG
GGGCTAGCCTGACTCCAGAACTTTAAGACTTTCTCCCCACTGCCTTCTGCTGCAGCCCAAG
CAGGGAGTGTCCCCCTCCAGAAAGCATATCCAGATGAGTGGTACATTATATAAGGATTTTTT
TTTAAGTTGAAAACAACCTTTCTTTTCTTTTGTATGATGGTTTTTTTAACACAGTCATTAAAA
ATGTTTATAAATCAAAA

FIGURE 68

MGPGARLAALLAVLALGTGDPERAAARGDTFSALTSVARALAPERLLGLLRRYLRGEEARL
RDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVVHSLEASENIRALKDGYEKVE
QDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRVGTGSAITDLYSPKRLFSLTGDDCFQ
VGKVAYDMGDYYHAIPWLEEAVSLFRGSYGEWKTEDEASLEDALDHLAFAYFRAGNVSCALS
LSREFLLYSPDNKRMARNVLKYERLLAESPNHVVAEAVIQRPNI PHLQTRDTYEGLCQTLGS
QPTLYQIPSLYCSYETNSNAYLLLQPIRKEVIHLEPYIALYHDFVSDSEAQKIRELAEPWLQ
RSVVASGEKQLQVEYRISKSAWLKDTVDPKLVTNLNHRIAALTGLDVRPPYAEYLQVVNYGIG
GHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLSSVEAGGATAFIYANLSVPVVRNAALFWW
NLHRSGEGDSDTLHAGCPVLVGDKWVANKWIEHYGQEFRRPCSSSPED

Signal peptide:

amino acids 1-19

FIGURE 69

GAGATAGGGAGTCTGGGTTTAAAGTTCCTGCTCCATCTCAGGAGCCCCTGCTCCCACCCCTAG
 GAAGCCACCAGACTCCACGGTGTGGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCC
 ACGAGCGCTGGCTGAGGGACCGAGCCGGAGAGCCCCGGAGCCCCCGTAACCCGCGCGGGGAG
 CGCCCAGGATGCCGCGCGGGGACTCGGAGCAGGTGCGCTACTGCGCGCGCTTCTCCTACCTC
 TGGCTCAAGTTTTCACTTATCATCTATTCCACCGTGTTCTGGCTGATTGGGGCCCTGGTCCT
 GTCTGTGGGCATCTATGCAGAGGTTGAGCGGCAGAAATATAAAACCCTTGAAAGTGCCTTCC
 TGGCTCCAGCCATCATCCTCATCCTCCTGGGCGTCGTCATGTTTCATGGTCTCCTTCATTGGT
 GTGCTGGCGTCCCTCCGTGACAACCTGTACCTTCTCCAAGCATTTCATGTACATCCTTGGGAT
 CTGCCTCATCATGGAGCTCATTGGTGGCGTGGTGGCCTTGACCTTCCGGAACCAGACCATTG
 ACTTCCTGAACGACAACATTTCGAAGAGGAATTGAGAACTACTATGATGATCTGGACTTCAAA
 AACATCATGGACTTTGTTCAGAAAAAGTTCAAGTGCTGTGGCGGGGAGGACTACCGAGATTG
 GAGCAAGAATCAGTACCACGACTGCAGTGCCCCCTGGACCCCTGGCCTGTGGGGTGCCCTACA
 CCTGCTGCATCAGGAACACGACAGAAGTTGTCAACACCATGTGTGGCTACAAAACATCGAC
 AAGGAGCGTTTCAGTGTGCAGGATGTATCTACGTGCGGGGCTGCACCAACGCCGTGATCAT
 CTGGTTTCATGGACAACCTACCCATCATGGCGTGCATCCTCCTGGGCATCCTGCTTCCCCAGT
 TCCTGGGGGTGCTGCTGACGCTGCTGTACATCACCCGGGTGGAGGACATCATCATGGAGCAC
 TCTGTCACTGATGGGCTCCTGGGGCCCCGGTGCCAAGCCCAGCGTGGAGGCGGCAGGCACGGG
 ATGCTGCTTGTGCTACCCCAATTAGGGGCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTC
 TGGGATAGCACCTCTCAGTCAACATCGTGGGGCTGGACAGGGCTGCGGGCCCCCTCTGCCCACA
 CTCAGTACTGACCAAAGCCAGGGCTGTGTGTGCCTGTGTGTAGGTCCCACGGCCTCTGCCTC
 CCCAGGGAGCAGAGCCTGGGCCTCCCCTAAGAGGCTTTCCCCGAGGCAGCTCTGGAATCTGT
 GCCCACCTGGGGCCTGGGGAACAAGGCCCTCCTTTCTCCAGGCCTGGGCTACAGGGGAGGGA
 GAGCCTGAGGCTCTGCTCAGGGCCCATTTTCATCTCTGGCAGTGCCCTTGGCGGTGGTATTCAA
 GGCAGTTTTGTAGCACCTGTAATTGGGGAGAGGGAGTGTGCCCTCGGGGCAGGAGGGAAGG
 GCATCTGGGGAAGGGCAGGAGGGAAGAGCTGTCCATGCAGCCACGCCCATGGCCAGGTTGGC
 CTCTTCTCAGCCTCCCAGGTGCCTTGAGCCCTCTTGCAAGGGCGGCTGCTTCCTTGAGCCTA
 GTTTTTTTTTTACGTGATTTTTGTAAACATTCATTTTTTTGTACAGATAACAGGAGTTTCTGAC
 TAATCAAAGCTGGTATTTCCCCGCATGTCTTATTCTTGCCCTTCCCCCAACCAGTTTGTAA
 TCAAACAATAAAAAACATGTTTTGTTTTGTTTTTAAAAAAA

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FIGURE 70

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863

><subunit 1 of 1, 294 aa, 1 stop

><MW: 33211, pI: 5.35, NX(S/T): 3

MPRGDSEQVRYCARFSYLWLKFSLLIYSTVFWLIGALVLSVGIYAEVERQKYKTLES AFLAP
AIILILLGVVMFMVSFIGV LASLRDNL YLLQAFMYILGICLIMELIGGVVALTFRNQTIDFL
NDNIRRG IENYYDDLDFKNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPG PLACGVPYTCC
IRNTTEVVNTMCGYKTIDKERFSVQDVIIYVRGCTNAV IIFMDNYTIMACILLGILLPQFLG
VLLTLLYITRVEDIIMEHSVTDG LLGPGAKPSVEAAGTGCCLCYPN

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 22-42, 57-85, 93-116, 230-257

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FIGURE 71

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGA
 CACCTGGGAAG**ATG**GCCGGCCCGTGACCTTCACCCTTCTCTGTGGTTTGCTGGCAGCCACC
 TTGATCCAAGCCACCCTCAGTCCCAGTGCAGTTCTCATCCTCGGCCCCAAAAGTCATCAAAGA
 AAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGC
 TCAGTGCCATGCGGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACC
 GTCCTGAAGCACATCATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAA
 GCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCA
 ACACGCCCCCTGGTCAAGACCATCGTGGAGTTCCACATGACGACTGAGGCCCAAGCCACCATC
 CGCATGGACACCAGTGCAAGTGGCCCCACCCGCCTGGTCCTCAGTGAAGTGTGCCACCAGCCA
 TGGGAGCCTGCGCATCCAAGTGTGTATAAGCTCTCCTTCCTGGTGAACGCCTTAGCTAAGC
 AGGTCATGAACCTCCTAGTGCCATCCCTGCCCAATCTAGTGAAAAACCAGCTGTGTCCCGTG
 ATCGAGGCTTCCTTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCCATTTTC
 CCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTATCCTGCCATCAAGGGTGACACCATTC
 AGCTCTACCTGGGGGCCAAGTTGTTGGACTCACAGGGAAAGGTGACCAAGTGGTTCAATAAC
 TCTGCAGCTTCCCTGACAATGCCCCACCCTGGACAACATCCCGTTTCAGCCTCATCGTGAGTCA
 GGACGTGGTGAAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGAATTCATGGTCCTGTTGG
 ACTCTGTGCTTCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGCTGATCAATGAAAAG
 GCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCCGAGTT
 TTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGCTGGAAGTGTTTCCCTCCA
 GTGAAGCCCTCCGCCCTTTGTTTACCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGTTTTTAC
 ACCAAAGGTGACCAACTTATACTCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTGAT
 GAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCC
 ACTCCATCCTGCTGCCGAACCAGAAATGGCAAATTAAGATCTGGGGTCCCAGTGTCATTGGTG
 AAGGCCTTGAGATTGAGGCAGCTGAGTCCCTCACTGACCAAGGATGCCCTTGTGCTTACTCC
 AGCCTCCTTGTGGAAACCCAGCTCTCCTGTCTCCCAG**TGA**AGACTTGGATGGCAGCCATCAG
 GGAAGGCTGGGTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAAT
 CAATAAACACTTGCCTGTGAAAAA

FIGURE 72

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881

><subunit 1 of 1, 484 aa, 1 stop

><MW: 52468, pI: 7.14, NX(S/T): 3

MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILOQLPLLSAM
REKPAGGIPVLGSLVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPL
VKTIVEFHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMN
LLVPSLPNLVKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDTIQLYL
GAKLLDSQGKVTWKFNNSAASLTMPITLDNIPFSLIVSQDVVKAAVAVALSPEEFMVLLDSVL
PESAHRLKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSSEAL
RPLFTLGIEASSEAQFYTKGDQLILNLNNISSDRIQLMNSGIGWFPDVLKNIITEIIHSIL
LPNONGKLRSGVPVSLVKALGFEEAESSLTKDVLVLTASLWKPSSPVSQ

Important features of the protein:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

FIGURE 73

GAGCGAAC**ATG**GCAGCGCGTTGGCGGTTTTGGTGTGTCTCTGTGACCATGGTGGTGGCGCTG
 CTCATCGTTTTGCGACGTTCCCTCAGCCTCTGCCCCAAAGAAAGAAGGAGATGGTGTATCTGA
 AAAGGTTAGTCAGCTGATGGAATGGACTAACAAAAGACCTGTAATAAGAATGAATGGAGACA
 AGTTCGGTCGCCTTGTGAAAGCCCCACCGAGAAATTACTCCGTTATCGTCATGTTCACTGCT
 CTCCAAGTGCATAGACAGTGTGTCGTTTTGCAAGCAAGCTGATGAAGAATTCCAGATCCTGGC
 AAACCTCCTGGCGATACTCCAGTGCATTACCAACAGGATATTTTTTGGCCATGGTGGATTTTG
 ATGAAGGCTCTGATGTATTTTCTAGATGCTAAACATGAATTCAGCTCCAACCTTTCATCAACTTT
 CCTGCAAAAGGGAAACCCAAACGGGGTGATACATATGAGTTACAGGTGCGGGGTTTTTCAGC
 TGAGCAGATTGCCCCGTGGATCGCCGACAGAACTGATGTCAATATTAGAGTGATTAGACCCC
 CAAATTATGCTGGTCCCCCTTATGTTGGGATTGCTTTTGGCTGTTATTGGTGGACTTGTGTAT
 CTTTGAAGAAGTAATATGGAATTTCTCTTTAATAAACTGGATGGGCTTTTGCAGCTTTGTG
 TTTTGTGCTTGCTATGACATCTGGTCAAATGTGGAACCATATAAGAGGACCACCATATGCCC
 ATAAGAATCCCCACACGGGACATGTGAATTATATCCATGGAAGCAGTCAAGCCCAGTTTGTA
 GCTGAAACACACATTGTTCTTCTGTTAATGGTGGAGTTACCTTAGGAATGGTGCCTTTATG
 TGAAGCTGCTACCTCTGACATGGATATTGGAAAGCGAAAGATAATGTGTGTGGCTGGTATTG
 GACTTGTTGTATTATTCTTCAGTTGGATGCTCTCTATTTTTTAGATCTAAATATCATGGCTAC
 CCATACAGCTTTCTGATGAGT**TAA**AAAGGTCCCAGAGATATATAGACACTGGAGTACTGGAA
 ATTGAAAACGAAAATCGTGTGTGTTTGAAAAGAAGAATGCAACTTGTATATTTTGTATTAC
 CTCTTTTTTTCAAGTGATTTAAATAGTTAATCATTTAAACCAAGAAGATGTGTAGTGCCTTA
 ACAAGCAATCCTCTGTCAAAATCTGAGGTATTTGAAAATAATTATCCTCTTAACCTTCTCTT
 CCCAGTGAACTTTATGGAACATTTAATTTAGTACAATTAAGTATATTATAAAAAATTGTAAAA
 CTACTACTTTGTTTTAGTTAGAACAAAGCTCAAACTACTTTAGTTAACTTGGTCATCTGAT
 TTTATATTGCCTTATCCAAAGATGGGGAAAGTAAGTCCTGACCAGGTGTTCCCACATATGCC
 TGTTACAGATAACTACATTAGGAATTCATTCTTAGCTTCTTCATCTTTGTGTGGATGTGTAT
 ACTTTACGCATCTTTCCTTTTGAAGTAGAGAAATTATGTGTGTCATGTGGTCTTCTGAAAATG
 GAACACCATTTCTTCAGAGCACACGTCTAGCCCTCAGCAAGACAGTTGTTTTCTCCTCCTCCTT
 GCATATTTCTACTGCGCTCCAGCCTGAGTGATAGAGTGAGACTCTGTCTCAAAAAAAGTA
 TCTCTAAATACAGGATTATAATTTCTGCTTGAGTATGGTGTAACTACCTTGTATTTAGAAA
 GATTTTCAAGTTCATTCCATCTCCTTAGTTTTCTTTTAAAGGTGACCCATCTGTGATAAAAAATA
 TAGCTTAGTGCTAAAATCAGTGTAACCTTATACATGGCCTAAAATGTTTCTACAAATTAGAGT
 TTGTCACTTATTCCATTTGTACCTAAGAGAAAAATAGGCTCAGTTAGAAAAGGACTCCCTGG
 CCAGGCGCAGTGACTTACGCCTGTAATCTCAGCACTTTGGGAGGCCAAGGCAGGCAGATCAC
 GAGGTGAGGAGTTCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTCTACTAAAAATAT
 AAAAATTAGCTGGGTGTGGTGGCAGGAGCCTGTAATCCCAGCTACACAGGAGGCTGAGGCAC
 GAGAATCACTTGAACCTCAGGAGATGGAGGTTTTCAGTGAGCCGAGATCACGCCACTGCACTCC
 AGCCTGGCAACAGAGCGAGACTCCATCTCAAAAAAAAAAAAAA

FIGURE 74

MAARWRFWCVSVTMVVALLIVCDVPSASAQRKKEMVLSEKVSQLMEWTKRNPVIRMNGDKFR
RLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFAMVDFDEG
SDVFQMLNMNSAPTFINFPAKGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY
AGPLMLGLLLA VIGGLVYLRRSNMEFLENKTGWAF AALCFVLAMTSGQMWNHIRGPPYAHKN
PHTGHVNYIHGSSQAQFVAETHIVLLFNNGGVTLGMVLLCEAATSDMDIGKRKIMCVAGIGLV
VLFFSWMLSIFRSKYHGYPSFLMS

Signal peptide:

amino acids 1-29

Transmembrane domains:

amino acids 183-205, 217-237, 217-287, 301-321

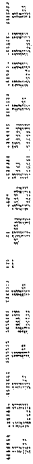


FIGURE 76

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885

<subunit 1 of 1, 536 aa, 1 stop

<MW: 61450, pI: 9.17, NX(S/T): 7

MLLLWVSVVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDFSFDGRLTFHPGSQVVKLPFINF
MKTRGTSFLNAYTNSPICCPSSRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQ
KFGKLDYTSGHHSISNRVEAWTRDVAFLLRQEGRPMVNLIRNRKVRVMERDWQNTDKAVNW
LRKEAINYTEPFVIYLGLNLPHYPSPSSGENFGSSTFHTSLYWLEKVSHDAIKIPKWSPLS
EMHPVDYYSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVIIY
SSDHGELAMEHRQFYKMSMYEASAHVPLLMMGPGIKAGLQVSNVVSIVDIYPTMLDIAGIPL
PQNLSGYSLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYS DGAS
ILPQLFDLSSDPDEL TNVAVKFPEITYSLDQKLHSIINYPKVSASVHQYNKEQFIKWKQSIG
QNYSNVIANLRWHQDWQKEPRKYENAI DQWLKTHMNPRAV

Important features:**Signal peptide:**

amino acids 1-15

N-glycosylation sites.

amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,
498-501

Sulfatases proteins:

amino acids 286-315, 359-369, 78-97

FIGURE 77

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG
AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCC**ATG**
GCCTCTCTTGGCCTCCAACCTTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACT
GGTTGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTTCGGTGCCAGCATTGTGACAG
CAGTTGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAG
TGTGACATCTATAGCACCCCTTCTGGGCCTGCCCCGCTGACATCCAGGCTGCCCAGGCCATGAT
GGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCA
CAGTCTTCTGCCAGGAATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTTC
ATCCTTGGAGGCCTCCTGGGATTCAATTCCTGTTGCCTGGAATCTTCATGGGATCCTACGGGA
CTTCTACTCACCCTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTTACTTGG
GCATTATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCCTGCTCATCC
CAGAGAAATCGCTCCAACCTACTACGATGCCTACCAAGCCCAACCTCTTGCCACAAGGAGCTC
TCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCCTACAGCCTGACAGGGT
ATGT**GTGA**AGAACCAGGGGCCAGAGCTGGGGGGTGGCTGGGTCTGTGAAAAACAGTGGACAG
CACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGTGTCAGAAGGTGCTGCTGAGG
ATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGGCTAGTGTAACAGCATG
CAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCTCACCTTGCTGCTC
CCCTGCCCTAAGTCCCCAACCCCTCAACTGAAACCCCATTCCTTAAGCCAGGACTCAGAGG
ATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACATCCCACTG
ACTGACCCTCTGTGATCAAAGACCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGG
GGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCC
TCCAAAGAACTGATTGGCCCTGGAACCTCCATCCCACTCTTGTTATGACTCCACAGTGTCC
AGACTAATTTGTGCATGAACTGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAG
GATGCAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

FIGURE 78

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886

><subunit 1 of 1, 230 aa, 1 stop

><MW: 24549, pI: 8.56, NX(S/T): 1

MASLGLQLVGYILGLLGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGIT
QCDIYSTLLGLPADIQAAQAMMVTSSAISLACIISVVGMRCTVFCQESRAKDRVAVAGGVF
FILGLLGFIPVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCS
SQNRNSNYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domains:

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

PMP-22 / EMP / MP20 family proteins.

amino acids 46-59

FIGURE 81

CTCCACTGCAACCACCCAGAGCCATGGCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATT
TTCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCT
GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCCTGCAGCACTGTT
GCTATGATGATGCCGTCGTGCCCTTGGCCAGGACCCAGACGTGTGGAACTGCACCTTCAGA
GTCTGCTTTGAGCAGTGCTGCCCCCTGGACCTTCATGGTGAAGCTGATAAACCAGAACTGCGA
CTCAGCCCCGGACCTCGGATGACAGGCTTTGTTCGAGTGTCAGCTAATGGAACATCAGGGGAA
CGATGACTCCTGGATTCTCCTTCCTGGGTGGGCCTGGAGAAAGAGGCTGGTGTACCTGAGA
TCTGGGATGCTGAGTGGCTGTTTGGGGGCCAGAGAAACACACACTCAACTGCCCCACTTCATT
CTGTGACCTGTCTGAGGCCCACCCTGCAGCTGCCCTGAGGAGGCCCACAGGTCCCCTTCTAG
AATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCCTCCTGAT
GACCCCTATGGCCAACATCAACCCGGCACCACCCCAAGGCTGGCTGGGGAACCCTTCACCCT
TCTGTGAGATTTTCCATCATCTCAAGTTCTCTTCTATCCAGGAGCAAAGCACAGGATCATAA
TAAATTTATGTACTTTATAAATGAAAA

FIGURE 82

MAPRGCIVAVFAIFCISRLLC SHGAPVAPMTPYLM LCQPHKRCGDKFYDPLQHCCYDDAVVP
LARTQTCGNCTFRVCFEQCCPWT FMVKLINQNCDSARTSDDRLCRSVS

Signal peptide:

amino acids 1-24

MAPRGCIVAVFAIFCISRLLC SHGAPVAPMTPYLM LCQPHKRCGDKFYDPLQHCCYDDAVVP
LARTQTCGNCTFRVCFEQCCPWT FMVKLINQNCDSARTSDDRLCRSVS

FIGURE 83

GGGGGCGGGTGCCTGGAGCACGGCGCTGGGGCCGCCCCGAGCGCTCACTCGCTCGCACTCAG
 TCGCGGGAGGCTTCCCCGCGCCGGCCGCGTCCCGCCCGCTCCCCGGCACCAGAAGTTCCTCT
 GCGCGTCCGACGGCGAC**ATG**GGCGTCCCCACGGCCCTGGAGGCCGGCAGCTGGCGCTGGGGA
 TCCCTGCTCTTCGCTCTCTTCCTGGCTGCGTCCCTAGGTCCGGTGGCAGCCTTCAAGGTCGC
 CACGCCGTATTCCCTGTATGTCTGTCCCGAGGGGCAGAACGTCACCCTCACCTGCAGGCTCT
 TGGGCCCTGTGGACAAAGGGCACGATGTGACCTTCTACAAGACGTGGTACCGCAGCTCGAGG
 GCGAGGTGCAGACCTGCTCAGAGCGCCGGCCCATCCGCAACCTCACGTTCCAGGACCTTCA
 CCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGCCACGACCTGGCTCAGCGCCACGGGC
 TGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGCAACCTGACCCTGCTG
 GATAGCGGCCTCTACTGCTGCCTGGTGGTGGAGATCAGGCACCACCACTCGGAGCACAGGGT
 CCATGGTGCCATGGAGCTGCAGGTGCAGACAGGCAAAGATGCACCATCCAAGTGTGTGGTGT
 ACCCATCCTCCTCCCAGGATAGTGAAAACATCACGGCTGCAGCCCTGGCTACGGGTGCCTGC
 ATCGTAGGAATCCTCTGCCTCCCCCTCATCCTGCTCCTGGTCTACAAGCAAAGGCAGGCAGC
 CTCCAACCGCCGTGCCAGGAGCTGGTGC GGATGGACAGCAACATTCAAGGGATTGAAAACC
 CCGGCTTTGAAGCCTCACCACCTGCCAGGGGATACCCGAGGCCAAAGTCAGGCACCCCTG
 TCCTATGTGGCCCAGCGGCAGCCTTCTGAGTCTGGGCGGCATCTGCTTTCGGAGCCCAGCAC
 CCCCCTGTCTCCTCCAGGCCCCGGAGACGTCTTCTTCCCATCCCTGGACCCTGTCCCTGACT
 CTCCAAACTTTGAGGTCATC**TAG**CCCAGCTGGGGGACAGTGGGCTGTTGTGGCTGGGTCTGG
 GGCAGGTGCATTTGAGCCAGGGCTGGCTCTGTGAGTGGCCTCCTTGGCCTCGGCCCTGGTTC
 CCTCCCTCCTGCTCTGGGCTCAGATACTGTGACATCCCAGAAGCCCAGCCCCTCAACCCCTC
 TGGATGCTACATGGGGATGCTGGACGGCTCAGCCCCTGTTCCAAGGATTTTGGGGTGTGAG
 ATTCTCCCCTAGAGACCTGAAATTCACCAGCTACAGATGCCAAATGACTTACATCTTAAGAA
 GTCTCAGAACGTCCAGCCCTTCAGCAGCTCTCGTTCTGAGACATGAGCCTTGGGATGTGGCA
 GCATCAGTGGGACAAGATGGACACTGGGCCACCCTCCCAGGCACCAGACACAGGGCACGGTG
 GAGAGACTTCTCCCCCGTGGCCGCTTGGCTCCCCCGTTTTGCCCCAGGCTGCTCTTCTGTC
 AGACTTCCTCTTTGTACCACAGTGGCTCTGGGGCCAGGCCTGCCTGCCCCTGGCCATCGCC
 ACCTTCCCCAGCTGCCTCCTACCAGCAGTTTCTCTGAAGATCTGTCAACAGGTTAAGTCAAT
 CTGGGGCTTCCACTGCCTGCATTCCAGTCCCCAGAGCTTGGTGGTCCCGAAACGGGAAGTAC
 ATATTGGGGCATGGTGGCCTCCGTGAGCAAATGGTGTCTTGGGCAATCTGAGGCCAGGACAG
 ATGTTGCCCCACCCACTGGAGATGGTGTGCTGAGGGAGGTGGGTGGGGCCTTCTGGGAAGGTGA
 GTGGAGAGGGGCACCTGCCCCCGCCCTCCCCATCCCCTACTCCCACTGCTCAGCGCGGGCC
 ATTGCAAGGGTGCCACACAATGTCTTGTCCACCCTGGGACACTTCTGAGTATGAAGCGGGAT
 GCTATTAAAACTACATGGGGAAAAAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

FIGURE 84

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897

><subunit 1 of 1, 311 aa, 1 stop

><MW: 33908, pI: 6.87, NX(S/T): 6

MGVPTALEAGSWRWGSLLFALFLAASLGPVAAFVKVATPYSLYVCPEGQNVTLTCRLLGPVDK
GHDVTFYKTWYRSSRGEVQTCSERRPIRNLTFQDLHLHHGGHQAANTSHDLAQRHGLEASD
HHGNFSITMRNLTLDDSGLYCCLVVEIRHHHSEHRVHGAMELQVQTGKDAPSNCVVYPSSSQ
DSENITAAALATGACIVGILCLPLILLVYKQRQAASNRRRAQELVRMDSNIQGIENPGFEAS
PPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSPPGPGDVFFPSLDPVPDSPNFEVI

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 190-216

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FIGURE 86

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902

><subunit 1 of 1, 451 aa, 1 stop

><MW: 49675, pI: 7.15, NX(S/T): 1

MVPEVRVLSSLLGLALLWFPLDSHARARPD MFCLFHGKRYSPGESWHPYLEPQGLMYCLRCT
CSEGAHVSCYRLHCPPVHCPQPVTEPQQCCPKC VEPHTPSGLRAPPKSCQHNGTMYQHGEIF
SAHELFPSRLPNQCVLC SCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEED
SVQSLHGVRHPQDPCSSDAGRKRGP GTPAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKH
KKACVHGGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPT EYPCRHPK VAGKC
CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKL V
KDEETEAQRGEVPGPRPHSQNLPLDSDQESQEARLPERGTALPTARWPPRRSLERLPSDPG
AEGHGQSRQSDQDITKT

Signal peptide:

amino acids 1-25

FIGURE 88

MDSLRLKMLISVAMLGAGAGVGYALLVIVTPGERRRKQEMLKEMPLQDPRSREEAARTQQLLLA
TLQEAATTQENVAWRKNWMVGEGGASGRSP

Signal peptide:

amino acids 1-18

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FIGURE 89

[illegible]

FIGURE 90

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905

<subunit 1 of 1, 406 aa, 1 stop

<MW: 46038, pI: 6.50, NX(S/T): 2

MGPSTPLLLILFLLSWSGPLQGQHHLVEYMERRLAALAEERLAQCQDQSSRHAAELRDFKNKM
LPILLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKGKGR
RNEKYDMVTDCGYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPRL
RDFTLAMAARKASRVRVPFPWVG TGQLVYGGFLYFARRPPGRPGGGGEMENTLQLIKFHLAN
RTVVDSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCCLAKLDPQTLDTQ
QWDTPCPRENAEAAAFVICGTLYVVYNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAH
ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEEV

Important features:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 177-180, 248-251

FIGURE 91

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCCTCCGCTCACGCAG
 AGCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTTCTCTAATCCAT
 CCGTCACCTCTCCTGTCATCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCC**ATGG**
 CTCTCATGCTCAGTTTGGTTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTT
 GGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGGAGGACGCAGCATTCTCCTGTTTCCTGTCT
 TCCTAAGACCAATGCAGAGGGCCATGGAAGTGCGGTCTTCAGGGGCCAGTTCTCTAGCGTGG
 TCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATCAAGGCAGG
 AAAAACTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGGAAAACATTAC
 TGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCCAGTCTTACTACCAGAAGGCCA
 TCTGGGAGCTACAGGTGTCAGCACTGGGCTCAGTTCCTCTCATTTCATCACGGGATATGTT
 GATAGAGACATCCAGCTACTCTGTCAGTCCCTCGGGCTGGTTCCCCCGGGCCACAGCGAAGTG
 GAAAGGTCCACAAGGACAGGATTTGTCCACAGACTCCAGGACAAACAGAGACATGCATGGCC
 TGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGAACGCCGGGAGCATATCCTGTTCCATG
 CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACTTTTTTCGA
 GCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTATTTTTTG
 GCATTGTTGGACTGAAGATTTTCTTCTCCAAATTCAGTGGAATCCAGGCGGAACCTGGAC
 TGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGGAAACACGCAGTGGAGGTGAC
 TCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAACCTGTAACCCATA
 GAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCT
 TCTCAGAGTTTCCAAGCAGGGAAACATTACTGGGAGGTGGACGGAGGACACAATAAAAGGTG
 GCGCGTGGGAGTGTGCCGGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTTGTCTCCCG
 ATCATGGGTACTGGGTCCTCAGACTGAATGGAGAACATTTGTATTTACATTAAATCCCCGT
 TTTATCAGCGTCTTCCCCAGGACCCACCTACAAAATAGGGGTCTTCCTGGACTATGAGTG
 TGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCCTGACATGTCGGT
 TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCCTATAATGAGCAAAATGGAACCTCCC
 ATAGTCATCTGCCCAGTCACCCAGGAATCAGAGAAAGAGGCCTCTTGGCAAAGGGCCTCTGC
 AATCCCAGAGACAAGCAACAGTGAGTCCTCCTCACAGGCAACCACGCCCTTCCTCCCCAGGG
 GTGAAATG**TAG**GATGAATCACATCCACATTCTTCTTTAGGGATATTAAGGTCTCTCTCCA
 GATCCAAAGTCCCGCAGCAGCCGGCCAAGGTGGCTTCCAGATGAAGGGGGACTGGCCTGTCC
 ACATGGGAGTCAGGTGTCATGGCTGCCCTGAGCTGGGAGGGAAGAAGGCTGACATTACATTT
 AGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGAAGAACCG
 TCAGGAATTCCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGC
 TTAGATCTTATTGATGACAGAGTGTATCCTAATGGTTTGTTCATTATATTACACTTTCAGTA
 AAAAA

FIGURE 92

MALMLSLVLSLLKLGSGQWQVFGPDKPVQALVGEDAAFSCFLSPKTNAEAMEVRFFRGQFSS
VVHLYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISSQSYQK
AIWELQVSALGSVPLISITGYVDRDIQLLCQSSGWFPRTAKWKGPQGQDLSTDSRTNRDMH
GLFDVEISLTVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF
FGIVGLKIFFSKFQWKIQAELDWRRKHGQAEIRDARKHAVEVTLPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFRTRKSVVASQS FQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTLS
PDHGYWVLRLNGEHLYFTLNPRFISVFPRTPPTKIGVFLDYECGTISFFNINDQSLIYTLTC
RFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASAI PETSNSESSSQATTPFLP
RGEM

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 239-255

CGCATGGGTGCGCCCGGTGGCGGTGGCGGCGGCGGTTGCGGAGGCTTCCTTGGTTCGATTGCA
ACGAGGAGAAGATGACTGACCAACCGACTGGCTGAATGAATGCGGAGCCGAGCGCGC
CATGAGGAGCCTGCCGAGCCTGGGCGGCCTCGCCCTGTTGTGCTGCGCCGCCGCCGCCGCCG
CCGTCGCCCTCAGCCGCCTCGGCGGGGAATGTCACCGGTGGCGGCGGGGCCGCCGGGGCAGGTG
GACGCGTCGCCGGGCCCGGGTTGCGGGGCGAGCCCAGCCACCCCTTCCCTAGGGCGACGGC
TCCCACGGCCCAGGCCCGAGGACCGGGCCCCCGCGCGCCACCGTCCACCGACCCCTGGCTG
CGACTTCTCCAGCCAGTCCCCGGAGACCACCCCTCTTTGGGCGACTGCTGGACCCCTCTTC
ACCACCTTTTCAGGCGCCGCTCGGCCCTCGCCGACCACCCCTCCGGCGGCGGAACGCACTTC
GACCACCTCTCAGGCGCCGACCAGCCCGCGCCGACCACCCCTTTCGACGACCACTGGCCCCG
CGCCGACCACCCCTGTAGCGACACCGTACCGGCGCCCCACGACTCCCCGGACCCCGACCCCT
GATCTCCCCAGCAGCAGCAACAGCAGCGTCTCTCCCCACCCACCTGCCACCGAGGCCCCCTC
TTCGCCCTCCTCCAGAGTATGTATGTAACCTGCTCTGTGGTTGGAAGCCTGAATGTGAATCGCT
GCAACCAGACCACAGGGCAGTGTGAGTGTGCGCCAGGTTATCAGGGGCTTCACTGTGAAACC
TGCAAAGAGGGCTTTTACCTAAATTACACTTCTGGGCTCTGTGAGCCATGTGACTGTAGTCC
ACATGGAGCTCTCAGCATACCGTGCAACAGG**TAA**GCAACAGAGGGTGGAAGTTTATT
TTATTTTATAGCAAGGGAAAAAAAAAAGGCTGCTACTCTCAAGGACCATACTGGTTTAAACAAAG
GAGGATGAGGGTCATAGATTTACAAATATTTTATATACTTTTATTCTCTTACTTTATATGT
TATATTTAATGTCAGGATTTAAAAACATCTAATTTACTGATTTAGTTCTTCAAAAGCACTAG
AGTCGCCAATTTTTCTCTGGGATAATTTCTGTAAATTTTCATGGGAAAAAATTATTGAAGAAT
AAATCTGCTTTCTGGAAGGGCTTTTCAGGCATGAAACCTGCTAGGAGGTTTAGAAATGTTCTT
ATGTTTATTAATATACCATTTGGAGTTTGAGGAAATTTGTTGTTTGGTTTATTTTTCTCTCTA
ATCAAAATTTCTACATTTGTTTCTTTGGACATCTAAAGCTTAACCTGGGGGTACCCTAATTTA
TTTAACTAGTGGAAGTAGACTGGTTTTTACTCTATTTACCAGTACATTTTTGAGACCAAAG
TAGATTAAGCAGGAATTATCTTTAAACTATTATGTTATTTGGAGGTAATTTAATCTAGTGGA
ATAATGTACTGTTATCTAAGCATTTGCCTTGTACTGCACTGAAAGTAATTATTTCTTTGACCT
TATGTGAGGCACCTTGGCTTTTTTGTGGACCCCAAGTCAAAAAACTGAAGAGACAGTATTAAT
AATGAAAAAATAATGACAGGTTATACTCAGTGTAACCTGGGTATAACCCAAGATCTGCTGC
CACTTACGAGCTGTGTTTCTTTGGGCAAGTAATTTCTTTCACTGAGCTTGTTTCTTCTCAAG
GTTGTTGTGAAGATTAAATGAGTTGATATATATAAAATGCCTAGCACATGTCACTCAATAAA
TTCTGGTTTTGTTTTAATTTCAAAGGAATATTATGGACTGAAATGAGAGAACATGTTTTAAGA
ACTTTTAGCTCCTTGACAAAGAAGTGCTTTTATACTTTAGCACTAAATATTTTTAAATGCTTTA
TAAATGATATTATACTGTTATGGAATATTGTATCATATTGTAGTTTATTAAAAATGTAGAAG
AGGCTGGGCGCGGTGGCTCACGCCTGTAATCCTAGCACTTTGGGAGGCCAAGGCGGGTGGAT
CACTTGAGGCCAGGAGTTCTAGATGAGCCTGGCCAGCACAGTGAAACCCCGTCTCTACTAAA
AATACAAACAAATTAGCTGGGCGTGGTGGCACACACCTGTAGTCCCAGCTACTCGGGAGGCT
GAGGCAGGAGAATCGGTTGAACCCGGGAGGTGGAGGTTGCAGTGAGCTGAGATCGCGCCACT
GCACTCCAGCCTGGTGAGAGAGGGGAGACTCTGTCTTAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 94

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952

><subunit 1 of 1, 258 aa, 1 stop

><MW: 25716, pI: 8.13, NX(S/T): 5

M R S L P S L G G L A L L C C A A A A A V A S A A S A G N V T G G G G A A G Q V D A S P G P G L R G E P S H P F P R A T A
P T A Q A P R T G P P R A T V H R P L A A T S P A Q S P E T T P L W A T A G P S S T T F Q A P L G P S P T T P P A A E R T S
T T S Q A P T R P A P T T L S T T T G P A P T T P V A T T V P A P T T P R T P T P D L P S S S N S S V L P T P P A T E A P S
S P P P E Y V C N C S V V G S L N V N R C N Q T T G Q C E C R P G Y Q G L H C E T C K E G F Y L N Y T S G L C Q P C D C S P
H G A L S I P C N R

Important features of the protein:**Signal peptide:**

amino acids 1-25

N-glycosylation sites.

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

EGF-like domain cysteine pattern signature.

amino acids 214-226.

FIGURE 95

TGCGGCGCAGTGTAGACCTGGGAGGATGGGCGGCCTGCTGCTGGCTGCTTTTCTGGCTTTGG
TCTCGGTGCCCAGGGCCCAGGCCGTGTGGTTGGGAAGACTGGACCCTGAGCAGCTTCTTGGG
CCCTGGTACGTGCTTGCGGTGGCCTCCCGGGAAAAGGGCTTTGCCATGGAGAAGGACATGAA
GAACGTCGTGGGGGTGGTGGTGACCCTCACTCCAGAAAACAACCTGCGGACGCTGTCCTCTC
AGCACGGGCTGGGAGGGTGTGACCAGAGTGTTCATGGACCTGATAAAGCGAAACTCCGGATGG
GTGTTTGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCCACCAACTTCAGAGA
CTATGCCATCATCTTCACTCAGCTGGAGTTCGGGGACGAGCCCTTCAACACCGTGGAGCTGT
ACAGTCTGACGGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTCACCAAGTGGAGCAGGAGC
CTGGGCTTCCTGTCACAGTAGCAGGCCCAGCTGCAGAAGGACCTCACCTGTGCTCACAAGAT
CCTTCTGTGAGTGCTGCGTCCCCAGTAGGGATGGCGCCACAGGGTCCTGTGACCTCGGCCA
GTGTCCACCCACCTCGCTCAGCGGCTCCCGGGGCCAGCACCAGCTCAGAATAAAGCGATT
CACAGCA

FIGURE 97

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCACAGACATGCTGCTGCTGCTGCTGCC
CCTGCTCTGGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTT
CCGTGACGGTGCAGGAAGGCCTGTGTGTCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCAT
GGCTGGATTTACCCTGGCCCAGTAGTTTCATGGCTACTGGTTCCGGGAAGGGGCCAATACAGA
CCAGGATGCTCCAGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACC
GATTCCACCTCCTTGGGGACCCACATACCAAGAATTGCACCCTGAGCATCAGAGATGCCAGA
AGAAGTGATGCGGGGAGATACTTCTTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAA
ACATCACCGGCTCTCTGTGAATGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCCAG
GCACCCTGGAGTCCGGCTGCCCCCAGAATCTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAG
GGGACACCCCCTATGATCTCCTGGATAGGGACCTCCGTGTCCCCCTGGACCCCTCCACCAC
CCGCTCCTCGGTGCTCACCCCTCATCCCACAGCCCCAGGACCATGGCACCCAGCCTCACCTGTC
AGGTGACCTTCCCTGGGGCCAGCGTGACCACGAACAAGACCGTCCATCTCAACGTGTCCTAC
CCGCCTCAGAACTTGACCATGACTGTCTTCCAAGGAGACGGCACAGTATCCACAGTCTTGGG
AAATGGCTCATCTCTGTCACTCCCAGAGGGCCAGTCTCTGCGCCTGGTCTGTGCAGTTGATG
CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCTGACCCTGTGCCCC
TCACAGCCCTCAAACCCGGGGGTGCTGGAGCTGCCTTGGGTGCACCTGAGGGATGCAGCTGA
ATTACCTGCAGAGCTCAGAACCCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCCCTGC
AGAGCAAAGCCACATCAGGAGTGACTCAGGGGGTGGTTCGGGGGAGCTGGAGCCACAGCCCTG
GTCTTCCTGTCCTTCTGCGTCATCTTCGTTGTAGTGAGGTCCTGCAGGAAGAAATCGGCAAG
GCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAAACGCTGTCAGGGGTTCAGCCT
CTCAGGGGCCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCCAGACCAGCCTCCCCCAGCT
TCTGCCCCGCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGT
GAAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCC
ACAGATTGAAAACTGCAGAGACTCACCCCTGATTGAGGGATCACAGCCCCTCCAGGCAAGGGA
GAAGTCAGAGGCTGATTCTTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACT
ATGAATTATGTGCAGAGTGAAAAGCACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAAT
CCACACTGTGCCCTCCCTTTTATTTTTTTAACTAAAAGACAGACAAATTCCTA

FIGURE 98

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSPSHGWIYPGPVVHGYWF
REGANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKG
SIKWNYPKHRLSVNVTALTHRPNILIPGTLESGCPQNLTCVWPWACEQGTTPPMISWIGTSVS
PLDPSTTRSSVLTLLIPQPQDHGTSLTCQVTFPGASVTTNKTVHLNVSYPPQNLTMTVFQGDG
TVSTVLGNGSSLSLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWV
HLRDAAEFTCRAQNPLGSQQVYLNVSLSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRS
CRKKSARPAAGVGDTGIEDANAVRGSSASQGPLEPWAEDSPPDQPPPASARSSVGEGELQYA
SLSFQMVKPWDSTRGQEATDTEYSEIKIHR

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 351-370

FIGURE 99

GACGCCCAGTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGAG**ATGA**AAGACCCTGTTTCCTG
GGTGTACGCTCGGCCTGGCCGCTGCCCTGTCCTTCACCCTGGAGGAGGAGGATATCACAGG
GACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTCCGGAGGACAGGAGGCCAGGA
AGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGTTACCTTC
ATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAGCCTGGCAA
ATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCCAGGAGGGACCACT
ACATCTTTTACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGGGAAAGCTTGTGGGT
AGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGG
ACTCTCGGAGGAGGACATTTTCACGCCCCTGCAGACGGGAAGCTGCGTTCCCGAACAC**TAGG**
CAGCCCCCGGGTCTGCACCTCCAGAGCCCACCCTACCACCAGACACAGAGCCCGGACCACCT
GGACCTACCCTCCAGCCATGACCCTTCCCTGCTCCCACCCACCTGACTCCAAATAAAGTCCT
TTTCCCCCAA

FIGURE 100

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65404

<subunit 1 of 1, 170 aa, 1 stop

<MW: 19457, pI: 9.10, NX(S/T): 0

MKTLFLGVTLGLAAALSFTLEEEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGGKL
EATFTFMREDRCIQKKILMRKTEEPGKYSAYGGRKLMYLQELPRRDHYIFYCKDQHHGGLLH
MGKLVGRNSDTNREALEEFKKLVQRKGLSEEDIFTPLQTGSCVPEH

Important features:**Signal peptide:**

amino acids 1-17

FIGURE 101

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCAC
AGCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCTCCAGGCC**ATG**AGGATTCTGCAGTTAA
TCCTGCTTGCTCTGGCAACAGGGCTTGTAGGGGGAGAGACCAGGATCATCAAGGGGTTCGAG
TGCAAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTGAGAAGACGCGGGCTACTCTGTGG
GGCGACGCTCATCGCCCCAGATGGCTCCTGACAGCAGCCCACTGCCTCAAGCCCCGCTACA
TAGTTCACCTGGGGCAGCACAACCTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAGCC
ACTGAGTCCTTCCCCCACCCCGGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGA
CATCATGCTGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCC
TCTCCTCACGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCCGGCTGGGGCAGCACGTCC
AGCCCCCAGTTACGCCTGCCTCACACCTTGCGATGCGCCAACATCACCATCATTGAGCACCA
GAAGTGTGAGAACGCCTACCCCGGCAACATCACAGACACCATGGTGTGTGCCAGCGTGCAGG
AAGGGGGCAAGGACTCCTGCCAGGGTGA CTCCGGGGGGCCCTCTGGTCTGTAACCAGTCTCTT
CAAGGCATTATCTCCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACAC
GAAAGTCTGCAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAAT**TAG**ACTGGACCCA
CCCACCACAGCCCATCACCTCCATTTCCACTTGGTGTGTTGGTTCCTGTTCACTCTGTTAAT
AAGAAACCCTAAGCCAAGACCCTCTACGAACATTCTTTGGGCCTCCTGGACTACAGGAGATG
CTGTCACTTAATAATCAACCTGGGGTTCGAAATCAGTGAGACCTGGATTCAAATTCTGCCTT
GAAATATTGTGACTCTGGGAATGACAACACCTGGTTTGTTCTCTGTTGTATCCCCAGCCCCA
AAGACAGCTCCTGGCCATATATCAAGGTTTCAATAAATATTTGCTAAATGAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 102

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405

<subunit 1 of 1, 250 aa, 1 stop

<MW: 27466, pI: 8.87, NX(S/T): 4

MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAH
 CLKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSITW
 AVRPLTLSSRCVTAGTSCGISGWGSTSSPQLRLPHTLRCANITIIIEHQKCENAYPGNITDTM
 VCASVQEGGKDSCQGDSSGGLVCNQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKNN

Important features:**Signal peptide:**

amino acids 1-18

Serine proteases, trypsin family, histidine active site.

amino acids 58-63

N-glycosylation sites.

amino acids 99-102, 165-168, 181-184, 210-213

Glycosaminoglycan attachment site.

amino acids 145-148

Kringle domain proteins.

amino acids 197-209, 47-64

Serine proteases, trypsin family, histidine protein

amino acids 199-209, 47-63, 220-243

Apple domain proteins

amino acids 222-249, 189-222

102/249

FIGURE 103

GAGCAGTGTTCTGCTGGAGCCG**ATG**CCAAAAACCATGCATTTCTTATTCAGATTCATTGTTT
TCTTTTATCTGTGGGGCCTTTTTACTGCTCAGAGACAAAAGAAAGAGGAGAGCACCGAAGAA
GTGAAAATAGAAGTTTTGCATCGTCCAGAAAACCTGCTCTAAGACAAGCAAGAAGGGAGACCT
ACTAAATGCCCATTTATGACGGCTACCTGGCTAAAGACGGCTCGAAATTCTACTGCAGCCGGA
CACAAAATGAAGGCCACCCCAAATGGTTTGTCTTGGTGTGGGCAAGTCATAAAAGGCCTA
GACATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGTAGTTATAACCCCTTCATT
TGCATACGGAAAGGAAGGCTATGCAGAAGGCAAGATTCACCGGATGCTACATTGATTTTTG
AGATTGAACTTTATGCTGTGACCAAAGGACCACGGAGCATTGAGACATTTAAACAAATAGAC
ATGGACAATGACAGGCAGCTCTCTAAAGCCGAGATAAACCTCTACTTGCAAAGGGAATTTGA
AAAAGATGAGAAGCCACGTGACAAGTCATATCAGGATGCAGTTTTAGAAAGATATTTTTAAGA
AGAATGACCATGATGGTGATGGCTTCATTTCTCCCAAGGAATACAATGTATACCAACACGAT
GAACTA**TAG**CATATTTGTATTTCTACTTTTTTTTTTTAGCTATTTACTGTACTTTATGTATA
AAACAAAGTCACTTTTCTCCAAGTTGTATTTGCTATTTTTCCCCTATGAGAAGATATTTTGA
TCTCCCCAATACATTGATTTTGGTATAATAAATGTGAGGCTGTTTTGCAAACCTTAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 104

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406

<subunit 1 of 1, 222 aa, 1 stop

<MW: 25794, pI: 6.24, NX(S/T): 1

MPKTMHFLFRFIVFFYLGWGLFTAQRQKKEESTEEVKIEVLHRPENCSKTSKKGDLLNAHYDG
YLAKDGSKFYCSRTQNEGHPKWFVLGVGQVIKGLDIAMTDMCPGKVRKVVIPPSFAYGKEGY
AEGKIPPDATLIFEIELYAVTKGPRSIETFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD
KSYQDAVLEDIFKKNDHGDGDFISPKEYNVYQHDEL

Important features:**Endoplasmic reticulum targeting sequence.**

amino acids 219-222

N-glycosylation site.

amino acids 45-48

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 87-223, 129-142

EF-hand calcium-binding domain proteins

amino acids 202-214, 195-214

FIGURE 105

CAGAAATGCAGGGACCATTGCTTCTTCCAGGCCTCTGCTTTCTGCTGAGCCTCTTTGGAGCT
GTGACTCAGAAAACCAAACTTCCTGTGCTAAGTGCCCCCAAATGCTTCCTGTGTCAATAA
CACTCACTGCACCTGCAACCATGGATATACTTCTGGATCTGGGCAGAACTATTCACATTCC
CCTTGGAGACATGTAACGCCAGGCATGGTGGCTCGCGCCTGTAATCCCAGTTCTTTGGGAAG
CCAAGGCAGGTGGATCACCTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATAGTGAAAC
CCCGTGTCTACTAAAAATACAAAATCAGCCGGGCGTGGTGGTGCATGCCTGCAATCCCAGT
TACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCTCAGGAGGCAGAAGTTGCAGTGAACCC
AGATCCTGCCATTGCACTCCAGCATGGATGACAGAGCAAGACTCCGTCTCAAAAAGAAAAGA
TAGTTTCTTGTTTCATTTTCGCGACTGCCCTCTCAGTGTTTCCTGGGATCCCCTCCCAAATAA
AGTACTTATATTCTC

105/249

FIGURE 106

MQGPLLLPGLCFLLSLFGAVTQKTKTSCAKCPPNASCVNNTHTCTCNHGYTSGSGQKLFTFPL
ETCNARHGG SRL

Signal peptide:

amino acids 1-18

106/249

FIGURE 107

CAAGCAGGTCATCCCCTTGGTGACCTTCAAAGAGAAGCAGAGAGGGCAGAGGTGGGGGGCAC
AGGGAAAGGGTGACCTCTGAGATTCCCCTTTTCCCCCAGACTTTGGAAGTGACCCACCATGG
GGCTCAGCATCTTTTTGCTCCTGTGTGTTCTTGGGCTCAGCCAGGCAGCCACACCGAAGATT
TTCAATGGCACTGAGTGTGGGCGTAACTCACAGCCGTGGCAGGTGGGGCTGTTTGAGGGCAC
CAGCCTGCGCTGCGGGGGTGTCTTATTGACCACAGGTGGGTCTCACAGCGGCTCACTGCA
GCGGCAGCAGGTACTGGGTGCGCCTGGGGGAACACAGCCTCAGCCAGCTCGACTGGACCGAG
CAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCCGGCTACCTGGGAGCCTCGACGAGCCA
CGAGCACGACCTCCGGCTGCTGCGGCTGCGCCTGCCCCTCCGCGTAACCAGCAGCGTTCAAC
CCCTGCCCCCTGCCCAATGACTGTGCAACCGCTGGCACCAGTGCCACGTCTCAGGCTGGGGC
ATCACCAACCACCCACGGAACCCATTCCCGGATCTGCTCCAGTGCCTCAACCTCTCCATCGT
CTCCCATGCCACCTGCCATGGTGTGTATCCCGGGAGAATCACGAGCAACATGGTGTGTGCAG
GCGGCGTCCCGGGGCAGGATGCCTGCCAGGGTGATTCTGGGGGCCCCCTGGTGTGTGGGGGA
GTCCTTCAAGGTCTGGTGTCTTGGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGG
AGTCTACACCTATATTTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACAACTGAC
CTGTTTCCTCCACCTCCACCCCCACCCCTTAACTTGGGTACCCCTCTGGCCCTCAGAGCACC
AATATCTCCTCCATCACTTCCCCTAGCTCCACTCTTGTGTCCTGGGAACTTCTTGGAACCT
TAACTCCTGCCAGCCCTTCTAAGACCCACGAGCGGGGTGAGAGAAGTGTGCAATAGTCTGGA
ATAAATATAAATGAAGGAGGGGCAAAAAAAAAAAAAA

FIGURE 108

MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAH
CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLRLPVRVTSSV
QPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVC
AGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSGVGPCGQDGIPGVYTYICKYVDWIRMIMRNN

Signal peptide:

amino acids 1-17

108/249

FIGURE 109

GCGGCCACACGCAGCTAGCCGGAGCCCGGACCAGGCGCCTGTGCCTCCTCCTCGTCCCTCGC
CGCGTCCGCGAAGCCTGGAGCCGGCGGGAGCCCCGCGCTCGCC**ATG**TCGGGCGAGCTCAGCA
ACAGGTTCCAAGGAGGGAAGGCGTTTCGGCTTGCTCAAAGCCCGGCAGGAGAGGAGGCTGGCC
GAGATCAACCGGGAGTTTCTGTGTGACCAGAAGTACAGTGATGAAGAGAACCTTCCAGAAAA
GCTCACAGCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCGAGATTGACC
TGATGTCTTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCCAAGACCCACCTGGAGATGAAG
AAGATGATCTCAGAGGTGACAGGAGGGGTGAGTACACTATATCCTACCGAGACTTTGTGAA
CATGATGCTGGGGAAACGGTCGGCTGTCCTCAAGTTAGTCATGATGTTTGAAGGAAAAGCCA
ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCCTCCAGAGAGAGACATTGCTAGCCTGCCC**TGA**
GGACCCCGCCTGGACTCCCCAGCCTTCCCACCCCATACCTCCCTCCCGATCTTGCTGCCCTT
CTTGACACACTGTGATCTCTCTCTCTCATTGTTTGGTCATTGAGGGTTTGTGTTGTGTTT
TCATCAATGTCTTTGTAAAGCACAAATTATCTGCCTTAAAGGGGCTCTGGGTGGGGAATCC
TGAGCCTTGGGTCCCCTCCCTCTCTTCTTCCCTCCTTCCCCGCTCCCTGTGCAGAAGGGCTG
ATATCAAACCAAAACTAGAGGGGGCAGGGCCAGGGCAGGGAGGCTTCCAGCCTGTGTTCCC
CTCACTTGGAGGAACCAGCACTCTCCATCCTTTCAGAAAGTCTCCAAGCCAAGTTCAGGCTC
ACTGACCTGGCTCTGACGAGGACCCCAAGGCACTCTGAGAAGACCTTGGAGTAGGGACAAGG
CTGCAGGGCCTCTTTCGGGTTTTCCTTGGACAGTGCCATGGTTCCAGTGCTCTGGTGTACCC
AGGACACAGCCACTCGGGGCCCCGCTGCCCCAGCTGATCCCCACTCATTCCACACCTCTTCT
CATCCTCAGTGATGTGAAGGTGGGAAGGAAAGGAGCTTGGCATTGGGAGCCCTTCAAGAAGG
TACCAGAAGGAACCCTCCAGTCTGCTCTCTGGCCACACCTGTGCAGGCAGCTGAGAGGCAG
CGTGCAGCCCTACTGTCCCTTACTGGGGCAGCAGAGGGCTTCGGAGGCAGAAGTGAGGCCTG
GGGTTTGGGGGGAAAGGTCAGCTCAGTGCTGTTCCACCTTTTAGGGAGGATACTGAGGGGAC
CAGGATGGGAGAATGAGGAGTAAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA
CTGAGAAATACAAGGTTGCTTGTCTGACCCCAATCTGCTTGAAAAAAAAAAAAAAAAAAAA

FIGURE 110

MSGELSNRFQGGKAFGLLKARQERRLAEGINREFLCDQKYSDEENLPEKLTAFKEKYMEFDLN
NEGEIDLMSLKRMMEKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVM
MFEGKANESSPKPVGPPPERDIASLP

110/249

FIGURE 111A

CGCGCTCCCCGCGCGCCTCCTCGGGCTCCACGCGTCTTGCCCCGCAGAGGCAGCCTCCTCCA
GGAGCGGGGCCCTGCACACC**ATG**GGCCCCCGGGTGGGCAGGGGTGCGCGCCGCCGTGCGCGCC
CGCCTGGCGCTGGCCTTGCGCTGGCGAGCGTCCTGAGTGGGCCTCCAGCCGTGCGCTGCCC
CACCAAGTGTACCTGCTCCGCTGCCAGCGTGGACTGCCACGGGCTGGGCCTCCGCGCGGGTTC
CTCGGGGCATCCCCGCAACGCTGAGCGCCTTGACCTGGACAGAAATAATATCACCAGGATC
ACCAAGATGGACTTCGCTGGGCTCAAGAACCTCCGAGTCTTGTCATCTGGAAGACAACCAGGT
CAGCGTCATCGAGAGAGGCGCCTTCCAGGACCTGAAGCAGCTAGAGCGACTGCGCCTGAACA
AGAATAAGCTGCAAGTCTTCCAGAATTGCTTTTCCAGAGCACGCCGAAGCTCACCAGACTA
GATTTGAGTGAAAACCAGATCCAGGGGATCCCGAGGAAGGCGTTCCGCGGCATCACCAGTGT
GAAGAACCTGCAACTGGACAACAACCACATCAGCTGCATTGAAGATGGAGCCTTCCGAGCGC
TGCGCGATTTGGAGATCCTTACCCTCAACAACAACAACATCAGTCGCATCCTGGTCACCAGC
TTCAACCACATGCCGAAGATCCGAACCTCTGCGCCTCCACTCCAACCACCTCTACTGCGACTG
CCACCTGGCCTGGCTCTCGGATTGGCTGCGACAGCGACGGACAGTTGGCCAGTTCACACTCT
GCATGGCTCCTGTGCATTTGAGGGGCTTCAACGTGGCGGATGTGCAGAAGAAGGAGTACGTG
TGCCCAGCCCCCACTCGGAGCCCCCATCCTGCAATGCCAACTCCATCTCCTGCCCTTCGCC
CTGCACGTGCAGCAATAACATCGTGGACTGTCGAGGAAAGGGCTTGATGGAGATTCTTGCCA
ACTTGCCGGAGGGGCATCGTCGAAATACGCCTAGAACAGAACTCCATCAAAGCCATCCCTGCA
GGAGCCTTCACCCAGTACAAGAACTGAAGCGAATAGACATCAGCAAGAATCAGATATCGGA
TATTGCTCCAGATGCCTTCCAGGGCCTGAAATCACTCACATCGCTGGTCTGTATGGGAACA
AGATCACCGAGATTGCCAAGGGACTGTTTGATGGGCTGGTGTCCCTACAGCTGCTCCTCCTC
AATGCCAACAAAGATCAACTGCCTGCGGGTGAACACGTTTCAGGACCTGCAGAACCTCAACTT
GCTCTCCCTGTATGACAACAAGCTGCAGACCATCAGCAAGGGGCTCTTCGCCCCCTCTGCAGT
CCATCCAGACACTCCACTTAGCCCCAAAACCCATTTGTGTGCGACTGCCACTTGAAGTGGCTG
GCCGACTACCTCCAGGACAACCCCATCGAGACAAGCGGGGCCCGCTGCAGCAGCCGCGCCG
ACTCGCCAACAAGCGCATCAGCCAGATCAAGAGCAAGAAGTTCCGCTGCTCAGGCTCCGAGG
ATTACCGCAGCAGGTTTCAGCAGCGAGTGCTTCATGGACCTCGTGTGCCCCGAGAAGTGTGCG
TGTGAGGGCACGATTGTGGACTGCTCCAACCAGAAGCTGGTCCGCATCCCAAGCCACCTCCC
TGAATATGTCACCGACCTGCGACTGAATGACAATGAGGTATCTGTTCTGGAGGCCACTGGCA
TCTTCAAGAAGTTGCCAACCTGCGGAAAATAAATCTGAGTAACAATAAGATCAAGGAGGTG
CGAGAGGGAGCTTTCGATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGACAGGGAACCAGCT
GGAGACCGTGCACGGGCGCGTGTTCGTGGCCTCAGTGGCCTCAAAACCTTGATGCTGAGGA
GTAACCTGATCAGCTGTGTGAGTAATGACACCTTTGCCGGCCTGAGTTCCGGTGAGACTGCTG
TCCCTCTATGACAATCGGATCACCACCATCACCCCTGGGGCCTTCACCACGCTTGTCTCCCT
GTCCACCATAAACCTCCTGTCCAACCCCTTCAACTGCAACTGCCACCTGGCCTGGCTCGGCA
AGTGGTTGAGGAAGAGGGCGGATCGTCAGTGGGAACCCTAGGTGCCAGAAGCCATTTTTCCTC
AAGGAGATTCCCATCCAGGATGTGGCCATCCAGGACTTCACCTGTGATGGCAACGAGGAGAG
TAGCTGCCAGCTGAGCCCGCGCTGCCCGGAGCAGTGCACCTGTATGGAGACAGTGGTGCAT
GCAGCAACAAGGGGCTCCGCGCCCTCCCCAGAGGCATGCCCAAGGATGTGACCGAGCTGTAC
CTGGAAGGAAACCACCTAACAGCCGTGCCAGAGAGCTGTCCGCCCTCCGACACCTGACGCT
TATTGACCTGAGCAACAACAGCATCAGCATGCTGACCAATTACACCTTCAGTAACATGTCTC
ACCTCTCCACTCTGATCCTGAGCTACAACCGGCTGAGGTGCATCCCCGTCCACGCCTTCAAC
GGGCTGCGGTCCCTGCGAGTGCTAACCTCCATGGCAATGACATTTCCAGCGTTCTGAAGG
CTCCTTCAACGACCTCACATCTCTTTCCCATCTGGCGCTGGGAACCAACCCACTCCACTGTG
ACTGCAGTCTTCGGTGGCTGTCGGAGTGGGTGAAGGCGGGGTACAAGGAGCCTGGCATCGCC
CGCTGCAGTAGCCCTGAGCCCATGGCTGACAGGCTCCTGCTCACCACCCCAACCCACCGCTT
CCAGTGCAAAGGGGCCAGTGGACATCAACATTGTGGCCAAATGCAATGCCTGCCTCTCCAGCC
CGTGCAAGAATAACGGGACATGCACCCAGGACCCTGTGGAGCTGTACCGCTGTGCCTGCCCC

FIGURE 111B

TACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCAACACCTGCATCCAGAACCCCTGTCA
GCATGGAGGCACCTGCCACCTGAGTGACAGCCACAAGGATGGGTTTCAGCTGCTCCTGCCCTC
TGGGCTTTGAGGGGCAGCGGTGTGAGATCAACCCAGATGACTGTGAGGACAACGACTGCGAA
AACAAATGCCACCTGCGTGGACGGGATCAACAACCTACGTGTGTATCTGTCCGCCTAACTACAC
AGGTGAGCTATGCGACGAGGTGATTGACCACTGTGTGCCTGAGCTGAACCTCTGTTCAGCATG
AGGCCAAGTGATCCCCCTGGACAAAGGATTGAGCTGCGAGTGTGTCCCTGGCTACAGCGGG
AAGCTCTGTGAGACAGACAATGATGACTGTGTGGCCACAAGTGCCGCCACGGGGGCCAGTG
CGTGGACACAATCAATGGCTACACATGCACCTGCCCCCAGGGCTTCAGTGGACCCTTCTGTG
AACACCCCCCACCCATGGTCCTACTGCAGACCAGCCCATGCGACCAGTACGAGTGCCAGAAC
GGGGCCCAAGTGATCGTGGTGCAGCAGGAGCCACCTGCCGCTGCCACCAGGCTTCGCCCG
CCCCAGATGCGAGAAGCTCATCACTGTCAACTTCGTGGGCAAAGACTCCTACGTGGAACCTGG
CCTCCGCCAAGGTCCGACCCCAGGCCAACATCTCCCTGCAGGTGGCCACTGACAAGGACAAC
GGCATCCTTCTCTACAAAGGAGACAATGACCCCCCTGGCACTGGAGCTGTACCAGGGGCCACGT
GCGGCTGGTCTATGACAGCCTGAGTTCCCCTCCAACCACAGTGTACAGTGTGGAGACAGTGA
ATGATGGGACAGTTTCACAGTGTGGAGCTGGTGCAGCTAAACCAGACCCTGAACCTAGTAGTG
GACAAAGGAACTCCAAAGAGCCTGGGGAAGCTCCAGAAGCAGCCAGCAGTGGGCATCAACAG
CCCCCTCTACCTTGGAGGCATCCCCACCTCCACCGGCCCTCTCCGCCTTGCGCCAGGGGCACGG
ACCGGCCTCTAGGCGGCTTCCACGGATGCATCCATGAGGTGCGCATCAACAACGAGCTGCAG
GACTTCAAGGCCCTCCCACCACAGTCCCTGGGGGTGTCAACAGGCTGCAAGTCCCTGCACCGT
GTGCAAGCACGGCCTGTGCCGCTCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGCCGCCAG
GCTGGACCGGCCCACTCTGCGACCAGGAGGCCCGGGACCCCTGCCTCGGCCACAGATGCCAC
CATGGAAAATGTGTGGCAACTGGGACCTCATACATGTGCAAGTGTGCCGAGGGCTATGGAGG
GGACTTGTGTGACAACAAGAATGACTCTGCCAATGCCTGCTCAGCCTTCAAGTGTCAACATG
GGCAGTGCCACATCTCAGACCAAGGGGAGCCCTACTGCCTGTGCCAGCCCGGCTTTAGCGGC
GAGCACTGCCAACAAGAGAATCCGTGCCTGGGACAAGTAGTCCGAGAGGTGATCCGCCGCCA
GAAAGGTTATGCATCATGTGCCACAGCCTCCAAGGTGCCCATCATGGAATGTGCTGGGGGCT
GTGGGGCCCCAGTGCTGCCAGCCCACCCGCAGCAAGCGGCGGAAATACGTCTTCCAGTGCACG
GACGGCTCCTCGTTTGTAGAAGAGGTGGAGAGACACTTAGAGTGCGGCTGCCTCGCGTGTTC
CTAAGCCCCCTGCCCGCCTGCCTGCCACCTCTCGGACTCCAGCTTGATGGAGTTGGGACAGCC
ATGTGGGACCCCCCTGGTGATTTCAGCATGAAGGAAATGAAGCTGGAGAGGAAGGTAAAGAAGA
AGAGAATATTAAGTATATTGTAAAAATAAACAAAAAATAGAACTTAAAAAAAAAAAAAAAAAA
AAAAAA

FIGURE 112

MAPGWAGVGAAVRARLALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGIPRN
 AERLDLDRNNITRITKMDFAGLKNLRVLHLEDNQVSVIERGAFQDLKQLERLRNLKNKLQVL
 PELLFQSTPKLTRLDLSENQIQGIPRKAFRGITDVKNLQLDNNHISCIEDGAFRALRDLEIL
 TLNNNNISRILVTSFNHMPKIRTLRLHSNHLYCDCHLAWLSDWLRQRRVTVGQFTLCMAPVHL
 RGFNVADVQKKEYVCPAPHSEPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPEGIV
 EIRLEQNSIKAIPAGAFTQYKKLKRIDISKNQISDIAPDAFQGLKSLTSLVLYGNKITEIAK
 GLFDGLVSLQLLLLNANKINCLRVNTFQDLQNLNLLSLYDNKLQTISKGLFAPLQSIQTLHL
 AQNPVCDCHLKWLDLYLQDNPIETSGARCSSPRRLANKRISQIKSKKFRCSGSEDYRSRFS
 SECFMDLVCPEKCRCEGTIVDCSNQKLVRIPSHLPEYVTDLRLNDNEVSVLEATGIFKKLPN
 LRKINLSNNKIKEVREGAFDGAASVQELMLTGNQLETVHGRVFRGLSGLKTLMLRSNLISCV
 SNDTFAGLSSVRLLSLYDNRIITTITPGAFTTLVSLSTINLLSNPFNCNCHLAWLGKWLKRKR
 IVSGNPRCQKPFLLKEIPIQDVAIQDFTCDGNEESSCQLSPRCPEQCTCMETVVRCSNKGRL
 ALPRGMPKDVTELYLEGNHILTAVPRELSALRHLLTIDLSNNSISMLTNYTFSNMSHLSTLIL
 SYNRLRCIPVHAFNGLRSLRVLT LHGNDISSVPEGSFNDLTSLSHLALGTNPLHDCDSLRLW
 SEWVKAGYKEPGIARCSSPEPMADRLLLTTPTHRFQCKGPVDINIVAKCNACLSSPCKNNGT
 CTQDPVELYRCACPYSYKGDCTVPINTCIQNPCQHGGTCHLSDSHKDGFSCSCPLGFEGQR
 CEINPDDCEDNDCENNATCVDGINNYVCICPPNYTGELCDEVIDHCVPELNLCQHEAKCIPL
 DKGFSCECVPGYSGLKCETDNDDCAHAKCRHGAQCVDTINGYTCTCPQGFSGPFCEHPPPMV
 LLQTSPCDQYECQNGAQCIVVQQEPTCRCPPGFAGPRCEKLITVNFVGKDSYVELASAKVRP
 QANISLQVATDKDNGILLYKGDNDPLALELYQGHVRLVYDSLSSPPTTVYSVETVNDGQFHS
 VELVTLNQTLNLVVDKGT PKSLGKLQKQPAVGINSPLYLGGIPTSTGLSALRQGTDRPLGGF
 HGCIEVRINNELQDFKALPPQSLGVSPGCKSCTVCKHGLCRSVEKDSVCECRPGWTGPLC
 DQEARDPCLGHRCHHGKCVATGTSYMCKCAEGYGGDLCDNKNDSANACSAFKCHHGQCHISD
 QGEPYCLCQPGFSGEHCQQENPCLGQVVREVIRROKGYASCATASKVPIMECRGGCGPQCCQ
 PTRSKRRKYVFQCTDGSSFVEEVERHLECGCLACS

Signal peptide:

amino acids 1-27

FIGURE 113

GGATGCAGGACGCTCCCCTGAGCTGCCTGTCACCGACTAGGTGGAGCAGTGTTTCTTCCGCA
GACTCAACTGAGAAGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTTCAGTTCTGTCT
CCGGCAGGCTTTGAGGATGAAGGCTGCGGGCATTCTGACCCTCATTGGCTGCCTGGTCACAG
GCGCCGAGTCCAAAATCTACACTCGTTGCAAACCTGGCAAAAATATTCTCGAGGGGCTGGCCTG
GACAATTACTGGGGCTTCAGCCTTGGAAACTGGATCTGCATGGCATATTATGAGAGCGGCTA
CAACACCACAGCCCCGACGGTCCTGGATGACGGCAGCATCGACTATGGCATCTTCCAGATCA
ACAGCTTCGCGTGGTGCAGACGCGGAAAGCTGAAGGAGAACAACCACTGCCATGTGCGCTGC
TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGA
GACACAAGGAATGAACTATTGGCAAGGCTGGAAGAAACATTGTGAGGGCAGAGACCTGTCCG
AGTGGAAAAAAGGCTGTGAGGTTTCCTAAACTGGAACCTGGACCCAGGATGCTTTGCAGCAAC
GCCCTAGGATTTGCAGTGAATGTCCAAATGCCTGTGTCATCTTGTCCCGTTTCCTCCCAATA
TTCCTTCTCAAACCTGGAGAGGGGAAAATTAAGCTATACTTTTAAGAAAATAAATATTTCCAT
TTAAATGTC

FIGURE 114

MKAAGILTLIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAP
TVLDDGSIDYGIFQINSFAWCRRGKCLKENNHCHVACSALITDDLTDALICARKIVKETQGMN
YWQGWKKHCEGRDLSEWKKKGCEVS

Signal peptide:

amino acids 1-19

115/249

FIGURE 115

CAGGCCATTTGCATCCCACTGCTGCTTGTGTTTCGGAGCCAGGCCACACCGTCCCTCAGCAGTGT
CATGTGTTAAAAACGCCAAGCTGAATATATCATGCCCCCTATTAAAACTTGTACATGGCTCCC
CATTGGTTTTTTGGAGAAAAGTTCAAGCTTTTTACCTTGGTGTCTGCCTGTATCCCAGTGTTC
AGGCTGGCTAGACGGCGGAAGAAGATCCTATTTTACTGTCACTTCCCAGATCTGCTTCTCAC
CAAGAGAGATTCTTTTCTTAAACGACTATACAGGGCCCCAATTGACTGGATAGAGGAATACA
CCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTCACAGCTGCTGTTTTTAAGGAA
ACATTCAAGTCCCTGTCTCACATAGACCCTGATGTCCTCTATCCATCTCTAAATGTCACCAG
CTTTGACTCAGTTGTTCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCCTGC
TGCTCTCCATCAACAGATACGAAAGGAAGAAAAATCTGACTTTGGCACTGGAAGCCCTAGTA
CAGCTGCGTGGAAGATTGACATCCCAAGATTGGGAGAGGGTTCATCTGATCGTGGCAGGTGG
TTATGACGAGAGAGTCTTGAGAATGTGGAACATTATCAGGAATTGAAGAAAATGGTCCAAC
AGTCCGACCTTGGCCAGTATGTGACCTTCTTGAGGTCTTTCTCAGACAAACAGAAAATCTCC
CTCCTCCACAGCTGCACGTGTGTGCTTTACACACCAAGCAATGAGCACTTTGGCATTGTCCC
TCTGGAAGCCATGTACATGCAGTGCCAGTCATTGCTGTAAATTCGGGTGGACCCTTGGAGT
CCATTGACCACAGTGTACAGGGTTTCTGTGTGAGCCTGACCCGGTGCACCTTCTCAGAAGCA
ATAGAAAAGTTCATCCGTGAACCTTCCTTAAAAGCCACCATGGGCCTGGCTGGAAGAGCCAG
AGTGAAGGAAAAAATTTCCCCTGAAGCATTTACAGAACAGCTCTACCGATATGTTACCAAAC
TGCTGGTATTAATCAGATTGTTTTTAAGATCTCCATTAATGTCATTTTTTATGGATTGTAGACC
CAGTTTTGAAACCAAAAAAGAAACCTAGAATCTAATGCAGAAGAGATCTTTTAAAAAATAAA
CTTGAGTCTTGAATGTGAGCCACTTTCCATATATACCACACCTCCCTGTCCACTTTTCAGAAA
AACCATGTCTTTTATGCTATAATCATTCCAAATTTTGCCAGTGTTAAGTTACAAATGTGGTG
TCATTCCATGTTTACGAGAGTATTTTAATTATATTTTCTCGGGATTATTGCTCTTCTGTCTA
TAAATTTTGAATGATACTGTGCCTTAATTGGTTTTTCATAGTTTAAGTGTGTATCATTATCAA
AGTTGATTAAATTTGGCTTCATAGTATAATGAGAGCAGGGCTATTGTAGTTCCCAGATTCAAT
CCACCGAAGTGTTCACTGTCATCTGTTAGGGAATTTTTGTTTGTCTGTCTTTGCCTGGATC
CATAGCGAGAGTGCTCTGTATTTTTTTTTTAAGATAATTTGTATTTTTTGCACACTGAGATATAA
TAAAGGTGTTTATCATAAAAA

FIGURE 116

MPLLKLVHGSPLVFG EKFKLFTLV SACIPV FRLARRRKKILFYCHFPDLLLT KRDSFLKRLY
RAPIDWIEEYTTGM ADCILVNSQFTA AVFKETFKSLSHIDPDVLYPSLNVTSFDSVVPEKLD
DLVPKGKKFLLLSIN RYERKKNLT LALEALVQLRGRLTSQDW ERVHLIVAGGYDERVLENVE
HYQELKKMVQQSDLG QYVTF LRSFSDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMQCPV
IAVNSGGPLESIDHSVTG FLCEPDVHFSEAIEKFIREPSLKATMGLAGRARVKEKFSPEAF
TEQLYRYVTKLLV

Signal peptide:

amino acids 1-15

117/249

FIGURE 117

GACTACGCCGATCCGAGACGTGGCTCCCTGGGCGGCAGAACC**ATG**TTGGACTTCGCGATCTT
 CGCCGTTACCTTCTTGCTGGCGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTTCCAGAC
 AAGCTGCAGGAATTCCAGGGATTACTCCAACCTGAAGAAAAAGATGGTAATCTTCCAGATATT
 GTGAATAGTGGAAGTTTGCATGAGTTCTGGTTAATTTGCATGAGAGATATGGGCCTGTGGT
 CTCCTTCTGGTTTGGCAGGCGCCTCGTGGTTAGTTTGGGCACTGTTGATGTACTGAAGCAGC
 ATATCAATCCCAATAAGACATCGGACCCTTTTGAAACCATGCTGAAGTCATTATTAAGGTAT
 CAATCTGGTGGTGGCAGTGTGAGTGAAAACCATGAGGAAAAAATTGTATGAAAATGGTGT
 GACTGATTCTCTGAAGAGTAACTTTGCCCTCCTCCTAAAGCTTTCAGAAGAATTATTAGATA
 AATGGCTCTCCTACCCAGAGACCCAGCACGTGCCCCTCAGCCAGCATATGCTTGGTTTTGCT
 ATGAAGTCTGTTACACAGATGGTAATGGGTAGTACATTTGAAGATGATCAGGAAGTCATTTCG
 CTTCCAGAAGAATCATGGCACAGTTTGGTCTGAGATTGGAAAAGGCTTTCTAGATGGGTCAC
 TTGATAAAAACATGACTCGGAAAAACAATATGAAGATGCCCTCATGCAACTGGAGTCTGTT
 TTAAGGAACATCATAAAAGAACGAAAAGGAAGGAAGTTCAGTCAACATATTTTCATTGACTC
 CTTAGTACAAGGGAACCTTAATGACCAACAGATCCTAGAAGACAGTATGATATTTTCTCTGG
 CCAGTTGCATAATAACTGCAAAATTGTGTACCTGGGCAATCTGTTTTTTAACCACCTCTGAA
 GAAGTTCAAAAAAATTATATGAAGAGATAAACCAAGTTTTTGGAAATGGTCCTGTACTCC
 AGAGAAAATTGAGCAGCTCAGATATTGTCAGCATGTGCTTTGTGAAACTGTTTGAAGTCCCA
 AACTGACTCCAGTTTCTGCCCAGCTTCAAGATATTGAAGGAAAAATTGACCGATTTATTATT
 CCTAGAGAGACCCTCGTCCTTTATGCCCTTGGTGTGGTACTTCAGGATCCTAATACTTGGCC
 ATCTCCACACAAGTTTGATCCAGATCGGTTTGATGATGAATTAGTAATGAAAACCTTTTTCCT
 CACTTGGATTCTCAGGCACACAGGAGTGTCCAGAGTTGAGGTTTGCATATATGGTGACCACA
 GTACTTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTTCTGTGGAGGGACAGGTTATTGA
 AACAAAGTATGAACTGGTAACATCATCAAGGGAAGAAGCTTGGATCACTGTCTCAAAGAGAT
 AT**TAA**AATTTTATACATTTAAAATCATTGTTAAATTGATTGAGGAAAACAACCATTTAAAAA
 AAATCTATGTTGAATCCTTTTATAAACAGTATCACTTTGTAATATAAACACCTATTTGTAC
 TTAA

FIGURE 118

MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLH
ERYGPVVSFWFGRRLLVVS LGTVDLKQHINPNKTS DPFETMLKSLRLRYQSGGGSVSENHMRK
KLYENGVTDSLKSNFALLKLSEELLDKWLSYPETQHVPLSQHMLGFAMKSVTQMVMGSTFE
DDQEVIRFQKNHGTWVSEIGKGFLDGS LDKNMTRKKQYEDALMQLESVLRNIIKERKGRNFS
QHIFIDSLVQGNLNDQQILED SMIFSLASCIITAKLCTWAICFLT TSEEVQKKLYEEINQVF
GNGPVTPEKIEQLRYCQHVL CETVRTAKLTPVSAQLQDIEGKIDRFIIPRETLVLYALGVVL
QDPNTWPSPHKFD PDRFDDELVMKTFSSLGFSGTQECPELRFAYMVTTVLLSVLVKRLHLLS
VEGQVIETKYELVTSSREEAWITVSKRY

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 271-290

FIGURE 119

CTAGATTTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACTTCCAGCCTCAGA
GACCGCCGCCCTTGTCCCCGAGGGGCC**ATG**GGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTC
CTGACGCTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCGGGACAGCAACAT
ACAGGCCTGCCTGCCTCTCACGTTACACCCCGAGGAGTATGACAAGCAGGACATTTCAGCTGG
TGGCCGCGCTCTCTGTACCCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCCTCTCAGGA
GTCTCCATGTTCAACAGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGT
GGCCCTGTCCTTCTTCATATTCGAGCGTTGGGAGTGCACCTACGTATTGGTACATTTTTGTCT
TCTGCAGTGCCCTTCCAGCTGTCACCTGAAATGGCTTTATTTCGTCACCGTCTTTGGGCTGAAA
AAGAAACCCTTC**TGA**TTACCTTCATGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGG
CCGCTTCGTATTCCTGGAAGAAGGAAGGCATAGGCTTCGGTTTTCCCTCGGAAACTGCTTC
TGCTGGAGGATATGTGTTGGAATAATTACGTCTTGAGTCTGGGATTATCCGCATTGTATTTA
GTGCTTTGTAATAAAATATGTTTTGTAGTAACATTAAGACTTATATACAGTTTTAGGGGACA
ATTAAAAAAAAAAAAA

FIGURE 120

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLG
LFAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCSALPAVT
EMALFVTVFGLKKKPF

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

121/249

FIGURE 121

TCCCGGACCCTGCCGCCCTGCCACT**ATG**TCCCGCCGCTCTATGCTGCTTGCCTGGGCTCTCC
CCAGCCTCCTTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCCTGCTGCAGCCCCATA
GTGCCCCGGAACGAGTGGAAGGCCCTGGCATCAGAGTGCGCCCAGCACCTGAGCCTGCCCTT
ACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGCTGCAACACCCCCGCCTCGTGCCAGC
AGCAGGCCCCGGAATGTGCAGCACTACCACATGAAGACACTGGGCTGGTGCACGTGGGCTAC
AACTTCCTGATTGGAGAAGACGGGCTCGTATACGAGGGCCGTGGCTGGAACCTTCACGGGTGC
CCACTCAGGTCACCTTATGGAACCCCATGTCCATTGGCATCAGCTTCATGGGCAACTACATGG
ATCGGGTGCCACACCCCAGGCCATCCGGGCAGCCCAGGGTCTACTGGCCTGCGGTGTGGCT
CAGGGAGCCCCTGAGGTCCAACCTATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTC
TCCAGGCAACCAGCTCTACCACCTCATCCAGAATTGGCCACACTACCGCTCCCCC**TGAG**GCC
CTGCTGATCCGCACCCCATTCCTCCCCTCCCATGGCCAAAAACCCCACTGTCTCCTTCTCCA
ATAAAGATGTAGCTC

122/249

FIGURE 122

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT
AGSSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP
MSIGISFMGNYMDRVPTPQAIRAAQGLLAGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL
IQNWPHYRSP

Signal peptide:

amino acids 1-20

123/249

FIGURE 123

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAG**ATG**CAACT
 GACTCGCTGCTGCTTCGTGTTCTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGG
 ATGATGGTCCTCCCGGCTCAGAGGACCCTGAGCGTGATGACCACGAGGGGCCAGCCCCGGCCC
 CGGGTGCTCGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCCATGGCCAATTCCACTCT
 CCTAGGGCTGCTGGCCCCGCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCC
 CGAACCACAGCCCCCACCCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTAC
 TCCAACATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGGAAGATTGTGGACCATGGCAA
 TGGGACCTTCAGCGTCCACTTCCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCC
 TCGTGCCCCCAGTAAAGCTGTAGAGTTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAG
 GCCTCCAAAATCTTCAACTGCCGGATGGAGTGGGAGAAGGTAGAACGGGGCCGCCGGACCTC
 GCTTTGCACCCACGACCCAGCCAAGATCTGCTCCCGAGACCACGCTCAGAGCTCAGCCACCT
 GGAGCTGCTCCCAGCCCTTCAAAGTCGTCTGTGTCTACATCGCCTTCTACAGCACGGACTAT
 CGGCTGGTCCAGAAGGTGTGCCCAGATTACAACCTACCATAGTGATACCCCCTACTACCCATC
 TGGG**TGA**CCCGGGGCAGGCCACAGAGGCCAGGCCAGGGCTGGAAGGACAGGCCTGCCCATGC
 AGGAGACCATCTGGACACCGGGCAGGGAAGGGGTGGGCCTCAGGCAGGGAGGGGGGTGGAG
 ACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAGAGAAAGGGTCCCAAGTG
 CTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGGAGGAGGAGTGGGCT
 CTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGGTCCCCGAGGCC
 TGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGCCCTTGTT
 CTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTTCATCAGTGTGGACAGCCTG
 TCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAGGAGCCAGTCAGCAGGGTGGGGTGGGGC
 CAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCCCTGTCTGTGCTGAGCATG
 GCATGAGGCTGAAGTGGCAACCCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTC
 CAGCCAGGCCACCCCTTTCCAAAATTCCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATT
 GCTGATGGCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCCTCCACACTAAGGCC
 ACAGCCCATCCGCGTGCTGTGTGTCCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAG
 CATCCATGTCCCGGAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTCAGACCGGGGTCTCTCC
 CGGATCTGGATGGCGCCGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGGCCGGGCCGAGA
 GCATGTGCTGGATCTGTTCTGTGTGTCTGTCTGTGGGTGGGGGAGGGGAGGGAAGTCTTGT
 GAAACCGCTGATTGCTGACTTTTGTGTGAAGAATCGTGTTCTTGGAGCAGGAAATAAAGCTT
 GCCCCGGGGCA

FIGURE 124

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521
><subunit 1 of 1, 252 aa, 1 stop
><MW: 28127, pI: 8.91, NX(S/T): 5
MQLTRCCFVFLVQGSLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMAN
STLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVD
HGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMWEKVERGR
RTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYRLVQKVCPDYNHSDTPY
YPSG

Important features of the protein:**Signal peptide:**

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

FIGURE 125

GTGAATGTGAGGGTTTGATGACTTTCAGATGTCTAGGAACCAGAGTGGGTGCAGGGGCCCCA
 GGCAGGGCTGATTCTTGGGCGGAGGAGAGTAGGGTAAAGGGTCTGCATGAGCTCCTTAAAG
 GACAAAGGTAACAGAGCCAGCGAGAGAGCTCGAGGGGAGACTTTGACTTCAAGCCACAGAAT
 TGGTGGAAGTGTGCGCGCCGCCGCCGCTCGCTCCTGCAGCGCTGTGACCTAGCCGCTAG
 CATCTTCCCGAGCACCGGGATCCCGGGGTAGGAGGCGACGCGGGCGAGCACCAGCGCCAGCC
 GGCTGCGGCTGCCACACGGCTCACC**ATG**GGCTCCGGGCGCCGGGCGCTGTCCGCGGTGCCG
 GCCGTGCTGCTGGTCCTCACGCTGCCGGGGCTGCCCGTCTGGGCACAGAACGACACGGAGCC
 CATCGTGCTGGAGGGCAAGTGTCTGGTGGTGTGCGACTCGAACCCGGCCACGGACTCCAAGG
 GCTCCTCTTCCCTCCCCGCTGGGGATATCGGTCCGGGCGGCCAACTCCAAGGTCGCCTTCTCG
 GCGGTGCGGAGCACCAACCACGAGCCATCCGAGATGAGCAACAAGACGCGCATCATTTACTT
 CGATCAGATCCTGGTGAATGTGGGTAATTTTTTTCACATTGGAGTCTGTCTTTGTAGCACCAA
 GAAAAGGAATTTACAGTTTCAGTTTTTCACGTGATTAAAGTCTACCAGAGCCAAACTATCCAG
 GTTAACTTGATGTTAAATGGAAAACCAGTAATATCTGCCTTTGCGGGGGACAAAGATGTTAC
 TCGTGAAGCTGCCACGAATGGTGTCTGCTCTACCTAGATAAAGAGGATAAGGTTTACCTAA
 AACTGGAGAAAGGTAATTTGGTTGGAGGCTGGCAGTATTCCACGTTTTCTGGCTTTCTGGTG
 TTCCCCCTA**TAG**GATTCAATTTCTCCATGATGTTTCATCCAGGTGAGGGATGACCCACTCCTG
 AGTTATTGGAAGATCATTTTTTTCATCATTGGATTGATGTCTTTTATTGGTTTTCTCATGGGTG
 GATATGGATTCTAAGGATTCTAGCCTGTCTGAACCAATACAAAATTTACAGATTATTTGTG
 TGTGTCTGTTTCAGTATATTTGGATTGGGACTCTAAGCAGATAATACCTATGCTTAAATGTA
 ACAGTCAAAAGCTGTCTGCAAGACTTATTCTGAATTTTCATTTCTGGGATTACTGAATTAGT
 TACAGATGTGGAATTTTATTTGTTTTAGTTTTTAAAGACTGGCAACCAGGTCTAAGGATTAGA
 AAACCTCTAAAGTTCTGACTTCAATCAACGGTTAGTGTGATACTGCCAAAGAACTGTATACTG
 TGTTAATATATTGATTATATTTGTTTTTATTCCTTTGGAATTAGTTTGTGTTGGTTCTTGTA
 AAACTTGGAATTTTTTTTTTTCAGTAACTGGTATTATGTTTTCTCTTAAATAAGGTAATGAA
 TGGCTTGCCCACAAATTTACCTTGACTACGATATCATCGACATGACTTCTCTCAAAAAAAAA
 GAATGCTTCATAGTTGTATTTTAATTGTATATGTGAAAGAGTCATATTTTCCAAGTTATATT
 TTCTAAGAAGAAGAATAGATCATAAATCTGACAAGGAAAAAGTTGCTTACCCAAAATCTAAG
 TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCCTCCGAGGGAAATCTTATACTTTATTGC
 TCAACTTTAATTAAAATGATTGATAATAACCACTTTATTAACCACTAAGGTTTTTTTTTTTT
 TCCGTAGACATGACCACTTTATTAACCTGGTGGTGGGATGCTGTTGTTTCTAATTATACCTAT
 TTTTCAAGGCTTCTGTTGTATTTGAAGTATCATCTGGTTTTGCCTTAACTCTTTAAATTGTA
 TATATTTATCTGTTTAGCTAATATTAAATTCAAATATCCCATATCTAAATTTAGTGCAATAT
 CTTGTCTTTTGTATAGGTCATATGAATTCATAAAATTATTTATGTCTGTTATAGAATAAAGA
 TTAATATATGTTAAAAAAA

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FIGURE 126

MSGRRALS AVPAVLLVLTLPGLPVWAQNDTEPIVLEGKCLVVCDSNPATDSKGSSSSPLGI
SVRAANSKVAFS AVRSTNHEPSEMSNKTRIIYFDQILVNVGNFFTLESVFVAPRKGIYSFSF
HVIKVYQSQTIQVNLMLNGKPVISAFAGDKDVTREAAATNGVLLYLDKEDKVYLLKLEKGNLVG
GWQYSTFSGFLVFPL

Signal peptide:

amino acids 1-27

127/249

FIGURE 127

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTC
GCCCTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGGAGC
TTTCTTCTGGTTGGTGTCTCTACTGATTTTCGTCCCTTGTTTGGTTCATGGCAAGAGTCATTA
TTGACAACAAAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTCTGTC
TATATCCAAGAAATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTT
GAAGAGTATAAACCCAGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTTCTGGCT
TGGGCTTTGGAATCATGAGTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTTGGGG
CCAGGCACAGTGGGCATTTCATGGAGATTCTCCTCAATTCTTCCTTTATTCAGCTTTCATGAC
GCTGGTCATTATCTTGCTGCATGTATTCTGGGGCATTGTATTTTTTGTATGGCTGTGAGAAGA
AAAAGTGGGGCATCCTCCTTATCGTTCTCCTGACCCACCTGCTGGTGTGAGCCAGACCTTC
ATAAGTTCTTATTATGGAATAAACCTGGCGTCAGCATTTATAATCCTGGTGTGCTCATGGGCAC
CTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTCTGCCAAG
ACAAGAACTTTCTTCTTTACAACCAGCGCTCCAGATAACCTCAGGGAACCAGCACTTCCCAA
ACCGCAGACTACATCTTTAGAGGAAGCACAACTGTGCCTTTTTTCTGAAAATCCCTTTTTCTG
GTGGAATTGAGAAAGAAATAAACTATGCAGATA

FIGURE 128

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658

><subunit 1 of 1, 257 aa, 1 stop

><MW: 28472, pI: 9.33, NX(S/T): 0

MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDN
KDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGF
GIMSGVFSFVNTLSDSLGPVTGVIHGDSPQFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKW
GILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSCLKCLLCQDKN
FLLYNQRSR

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

FIGURE 129

CGGCAACCAGCCGCCGCCACCACCGCTGCCACTGCCGCCCTGCCGGGGCC**ATG**TTTCGCTCTGGGCTTGCCCTTCT
 TGGTGCTCTTGGTGGCCTCGGTTCGAGAGCCATCTGGGGGTCTGGGGGCCAAGAACGTCTCGCAGAAAGACGCCG
 AGTTTTGAGCGCACCTACGTGGACGAGGTCAACAGCGAGCTGGTCAACATCTACACCTTCAACCATACTGTGACCC
 GCAACAGGACAGAGGGCGTGCCTGTGTCTGTGAACGCTCTGAACAAGCAGAAGGGGGCGCCGTTGCTGTTTGTGG
 TCCGCCAGAAGGAGGCTGTGGTGTCTTCCAGGTGCCCTAATCCTGCGAGGGATGTTTCAGCGCAAGTACCTCT
 ACCAAAAAGTGAACGAACCCCTGTGTACGCCCCCACCAGAATGAGTCGGAGATTTCAGTTCTTCTACGTGGATG
 TGTCCACCCTGTACACAGTCAACACCACATACCAGCTCCGGGTGAGCCGCATGGACGATTTTGTGCTCAGGACTG
 GGGAGCAGTTTCAGCTTCAATACCACAGCAGCAGCCCCAGTACTTCAAGTATGAGTTCCCTGAAGGCGTGGACT
 CGGTAATTGTCAAGGTGACCTCCAACAAGGCCTTCCCTGCTCAGTCATCTCCATTTCAGGATGTGCTGTGTCTG
 TCTATGACCTGGACAACAACGTAGCCTTTCATCGGCATGTACCAGACGATGACCAAGAAGGCGGCCATCACCGTAC
 AGCGCAAAGACTTCCCCAGCAACAGCTTTTATGTGGTGGTGGTGGTGAAGACCGAAGACCAAGCCTGCGGGGGCT
 CCCTGCCTTTTACCCCTTTCGAGAAAGATGAACCGGTGCGATCAAGGGCACCGCCAGAAAACCCCTGTGAGTGTGG
 TGTCTCAAGCAGTCACGTCTGAGGCATACGTGAGTGGGATGCTCTTTTGCCTGGGTATATTTCTCTCTCTTTTACC
 TGCTGACCGTCTCTGGCCTGCTGGGAGAAGTGGAGGCAGAAGAAGACCCCTGCTGGTGGCCATTGACCGAG
 CCTGCCAGAAAGCGGTCAACCTCGAGTCTGGCTGATTCTTTTCTGCGAGTTCCCTTATGAGGGTTACAAC
 ATGGCTCCTTTGAGAATGTTTCTGGATCTACCGATGGTCTGGTTGACAGCGCTGGCACTGGGGACCTCTCTTACG
 GTTACCAGGGCCGCTCCTTTGAACCTGTAGGTACTCGGCCCCGAGTGGACTCCATGAGCTCTGTGGAGGAGGATG
 ACTACGACACATTGACCGACATCGATTCCGACAAGAATGTCATTTCGCACCAAGCAATACCTCTATGTGGCTGACC
 TGGCAGGAAGGACAAGCGTGTCTGCGGAAAAAGTACCAGATCTACTTCTGGAACATTGCCACCATTGCTGTCT
 TCTATGCCCTTCTGTGGTGCAGCTGGTGATCACCTACCAGCGGTGGTGAATGTCACAGGGAATCAGGACATCT
 GCTACTACAACCTTCTCTGCGCCCACTGGGCAATCTCAGCGCCTTCAACAACATCCTCAGCAACCTGGGGT
 ACATCCTGCTGGGGCTGCTTTTCTGCTCATCATCTGCAACGGGAGATCAACCACAACCGGGCCCTGCTGCGCA
 ATGACCTCTGTGCCCTGGAATGTGGGATCCCCAAACACTTTGGGCTTTTCTACGCCATGGGCGACAGCCCTGATGA
 TGGAGGGGCTGCTCAGTGCTTGCTATCATGTGTGCCCAACTATAACCAATTTCCAGTTTGACACATCGTTTCATGT
 ACATGATCGCCGACTCTGCATGCTGAAGCTCTACCAGAAGCGGCACCCGGACATCAACGCCAGCGCCTACAGTG
 CCTACGCCCTGCCTGGCCATTGTCATCTTCTCTGTGTGGTGGGCTGGTCTTTGGCAAAGGGAACACGGCGTTCT
 GGATCGTCTTCTCCATCATTCACATCATCGCCACCCTGCTCCTCAGCACGCAGCTCTATTACATGGGCCGGTGGGA
 AACTGGACTCGGGGATCTTCCGCCGCATCTCCACGTGCTCTACACAGACTGCATCCGGCAGTGCAGCGGGCCGC
 TCTACGTGGACCGCATGGTGTGCTGGTTCATGGGCAACGTTCATCAACTGGTTCGCTGGCTGCCTATGGGCTTATCA
 TGCGCCCCAATGATTTTCGCTTCTCTACTTGTGGCCATTGGCATCTGCAACCTGCTCCTTTACTTTCGCTTCTACA
 TCATCATGAAGCTCCGGAGTGGGAGAGGATCAAGCTCATCCCCCTGCTCTGCATCGTTTGCACCTCCGTGGTCT
 GGGGCTTCGCGCTCTTCTTCTTCTCCAGGGACTCAGCACCTGGCAGAAAACCCCTGCAGAGTGCAGGGAGCACA
 ACCGGGACTGCATCCTCCTCGACTTCTTTGACGACCACGACATCTGGCACTTCTCTCCTCCATCGCCATGTTTCG
 GGTCTTCTGCTGGTGTGCTGACACTGGATGACGACCTGGATACTGTGCAGCGGGACAAGATCTATGTCTTCT**TAGC**
 AGGAGCTGGGCCCTTCGCTTCACTTCAAGGGGCCCTGAGCTCCTTTGTGTCTAGACCGGTCACTCTGTCTGTCT
 GTGGGGATGAGTCCCAGCACCGCTGCCAGCACTGGATGGCAGCAGGACAGCCAGGTCTAGCTTAGGCTTGGCCT
 GGGACAGCCATGGGGTGGCATGGAACCTTGCACTGCCCTCTGCCGAGGAGCAGGCCTGCTCCCCTGGAACCCCC
 AGATGTTGGCCAAATTGCTGCTTCTTCTCAGTGTGGGGCCTTCCATGGGGCCCTGTCTTTGGCTCTCCATTT
 GTCCCTTTGCAAGAGGAAGGATGGAAGGGACACCCTCCCCATTTTCATGCCTTGCATTTTGGCCGTCTCTCCCC
 ACAATGCCCCAGCCTGGGACCTAAGGCCTCTTTTCTCTCCATACTCCCACTCCAGGGCCTAGTCTGGGGCCTGA
 ATCTCTGTCTGTATCAGGGCCCCAGTTCTCTTTGGGCTGTCCTGGCTGCCATCACTGCCATTCCAGTCAGCC
 AGGATGGATGGGGGTATGAGATTTTGGGGGTGGCCAGCTGGTGCCAGACTTTTGGTGCTAAGGCCTGCAAGGGG
 CCTGGGGCAGTGCCTATTCTTCTTCTGACCTGTGCTCAGGGCTGGCTCTTTAGCAATGCGCTCAGCCCAATT
 TGAGAACCGCCTTCTGATTCAAGAGGCTGAATTCAGAGGTCACTCTTCATCCCATCAGCTCCAGACTGATGCC
 AGCACCAGGACTGGAGGGAGAAGCGCCTCACCCCTTCCCTTCTTTCCAGGGCCCTTAGTCTTGCCAAACCCC
 AGCTGGTGGCCTTTTCAGTGCCATTGACACTGCCCAAGAATGTCCAGGGGCAAAGGAGGGATGATACAGAGTTTCA
 CCCGTTCTGCCTCCACAGCTGTGGGCACCCAGTGCTACCTTAGAAAGGGGGCTTCAGGAAGGGATGTGCTGTTT
 CCCTCTACGTGCCAGTCTTAGCCTCGCTCTAGGACCCAGGGCTGGCTTCTAAGTTTCCGTCCAGTCTTTCAGGCA
 AGTTCTGTGTTAGTCATGCACACATACCTATGAAACCTTGGAGTTTACAAAGAATTGCCCCAGCTCTGGGCAC
 CCTGGCCACCCCTGGTCTTGGATCCCTTCGTCCCACCTGGTCCACCCAGATGCTGAGGATGGGGGAGCTCAGG
 CGGGCCCTCTGCTTTGGGGATGGGAATGTGTTTTCTCCAAACTTGTTTTTATAGCTCTGCTTGAAGGGCTGGG
 AGATGAGGTGGGTCTGGATCTTTTCTCAGAGCGTCTCCATGCTATGGTTGCATTTCCGTTTTCTATGAATGAATT
 TGCATTCAATAACAACCAGACTCAAAAAAAAAAAAAA

FIGURE 130

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659

><subunit 1 of 1, 832 aa, 1 stop

><MW: 94454, pI: 6.94, NX(S/T): 12

MFALGLPFLVLLVASVESH LGVLGPKNVSQKDAEFERTYVDEVNSELVNIYTFNHTVTRNRT
EGVRVSVNVLNKQKGAPLLFVVRQKEAVVSFQVPLILRGMFQRKYLYQKVERTLCQPPTKNE
SEIQFFYVDVSTLSPVNNTTYQLRVSRMDDFVLRTGEQFSFNTTAAQPQYFKYEFPEGVDSVI
VKVTSNKAFCPSVISIQDVLCPVYDLNNAVAFIGMYQTMTKKAAITVQRKDFPSNSFYVVVV
VKTEDQACGGS LFPYPFAEDEPVDQGHRQKTL SVLVSQAVTSEAYVSGMLFCLGIFLSFYLL
TVLLACWENWRQKKKTLLVAIDRACPESGHPRVLADSFPGSSPYEGYNYGSFENVSGSTDGL
VDSAGTGDLSYGYQGRSFEPVGT RPRVDSMSSVEEDDYDTLTDIDSDKNVIRTKQYLYVADL
ARKDKRVL RKKYQIYFWNIATIAVFYALPVVQLVITYQTVVNVVTGNQDICYYNFLCAHPLGN
LSAFNNILSNLGYILLG LLFLLIILQREINHN RALLRNDLCALECGIPKHFG LFYAMGTALM
MEGLLSACYHVC PNYTNFQFDTSFMYMIAGLCMLKLYQKRHPDINASAYSAYACLAIVIFFS
VLGVVFGKGNTAFWIVFSIIHIIATLLLSTQLYYMGRWKLD SGIFRRILHVLYTDCIRQCSG
PLYVDRMVLLVMGNVINWSLAAYGLIMRPNDFASYLLAIGICNLLLYFAFYIIMKLRSGERI
KLIPLLCIVCTSVVWGFALFFFFQGLSTWQKTPAESREHNRDCILLDFDDHDIWHFLSSIA
MFGSFLVLLTLDDDLDTVQRDKIYVF

Important features of the protein:**Signal peptide:**

amino acids 1-18

Transmembrane domains:

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

Leucine zipper pattern.

amino acids 497-518

N-glycosylation sites.

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

FIGURE 131

GCTCAAGTGCCCTGCCTTGCCCCACCCAGCCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC
 TCTCTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCCTGTCTTG
 ACC**ATG**GTCCTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCCAGGCTCTCCCCAAGGC
 CCAGCCTGCAGAGCTGTCTGTGGAAGTTCCAGAAAATATGGTGGAAATTTCCCTTTATACC
 TGACCAAGTTGCCGCTGCCCCGTGAGGGGGCTGAAGGCCAGATCGTGCTGTCAGGGGACTCA
 GGCAAGGCAACTGAGGGGCCATTTGCTATGGATCCAGATTCTGGCTTCCTGCTGGTGACCAG
 GGCCCTGGACCGAGAGGAGCAGGCAGAGTACCAGCTACAGGTACCCCTGGAGATGCAGGATG
 GACATGTCTTGTGGGGTCCACAGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAGGTG
 CCCCATTTCTCTCAAGCCATCTACAGAGCTCGGCTGAGCCGGGGTACCAGGCCTGGCATCCC
 CTTCTCTTCCCTTGAGGCTTCAGACCGGGATGAGCCAGGCACAGCCAACTCGGATCTTCGAT
 TCCACATCCTGAGCCAGGCTCCAGCCCAGCCTTCCCCAGACATGTTCCAGCTGGAGCCTCGG
 CTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACCAGCCTTGACCACGCCCTGGAGAGGAC
 CTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGACCAGGCCTCAGGCCACCAGGCCACTG
 CCACCGTGGAAGTCTCCATCATAGAGAGCACCTGGGTGTCCCTAGAGCCTATCCACCTGGCA
 GAGAATCTCAAAGTCCTATACCCGCACCACATGGCCCAGGTACACTGGAGTGGGGGTGATGT
 GCACTATCACCTGGAGAGCCATCCCCCGGGACCCCTTTGAAGTGAATGCAGAGGGAAACCTCT
 ACGTGACCAGAGAGCTGGACAGAGAAGCCCAGGCTGAGTACCTGCTCCAGGTGCGGGCTCAG
 AATTCCCATGGCGAGGACTATGCGGCCCTCTGGAGCTGCACGTGCTGGTGATGGATGAGAA
 TGACAACGTGCCTATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCTCAGTCCAC
 CAGGTACTGAAGTGAAGTAGACTGTGAGCAGAGGATGCAGATGCCCCCGGCTCCCCCAATTCC
 CACGTTGTGTATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTCCA
 GGTGGACCCCACTTCAGGCAGTGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAACA
 TCCTGCTTCTGGTGCTGGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCACGTGT
 GAAGTCGAAGTCGCAGTCACAGATATCAATGATCACGCCCTGAGTTCATCACTTCCCAGAT
 TGGGCCTATAAGCCTCCCTGAGGATGTGGAGCCCGGGACTCTGGTGGCCATGCTAACAGCCA
 TTGATGCTGACCTCGAGCCCGCCTTCCGCTCATGGATTTTGCCATTGAGAGGGGAGACACA
 GAAGGGACTTTTGGCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAA
 GAACCTCAGTTATGAGGCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGA
 AGCTGGTGGGGCCAGGCCCAGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGAGAGA
 GTGATGCCACCCCCAAGTTGGACCAGGAGAGCTACGAGGCCAGTGTCCCCATCAGTGCCCC
 AGCCGGCTCTTTCTGCTGACCATCCAGCCCTCCGACCCCATCAGCCGAACCCCTCAGGTTCT
 CCCTAGTCAATGACTCAGAGGGCTGGCTCTGCATTGAGAAATTCTCCGGGGAGGTGCACACC
 GCCCAGTCCCTGCAGGGCGCCCAGCCTGGGGACACCTACACGGTGCTTGTGGAGGGCCAGGA
 TACAGCCCTGACTCTTGCCCCCTGTGCCCTCCCAATACCTCTGCACACCCCGCCAAGACCATG
 GCTTGATCGTGAGTGGACCCAGCAAGGACCCCGATCTGGCCAGTGGGCACGGTCCCTACAGC
 TTCACCCTTGGTCCCAACCCACGGTGCAACGGGATTGGCGCCTCCAGACTCTCAATGGTTC
 CCATGCCTACCTCACCTTGGCCCTGCATTGGGTGGAGCCACGTGAACACATAATCCCCGTGG
 TGGTCAGCCACAATGCCCAGATGTGGCAGCTCCTGGTTCGAGTGATCGTGTGCTGCAAC
 GTGGAGGGGACAGTGCATGCGCAAGGTGGGCCGCATGAAGGGCATGCCACGAAGCTGTCCGC
 AGTGGGCATCCTTGTAGGCACCCTGGTAGCAATAGGAATCTTCCTCATCCTCATTTTACCC
 ACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGCCCTGAAGGCG
 ACTGTCT**TGA**ATGGCCCAGGCAGCTCTAGCTGGGAGCTTGGCCTCTGGCTCCATCTGAGTCCC
 CTGGGAGAGAGCCCAGCACCCAAGATCCAGCAGGGGACAGGACAGAGTAGAAGCCCCTCCAT
 CTGCCCTGGGGTGGAGGCACCATCACCATCACCAGGCATGTCTGCAGAGCCTGGACACCAAC
 TTTATGGACTGCCCATGGGAGTGCTCCAAATGTGAGGGTGTGTGCCCCAATAATAAAGCCCCA
 GAGAACTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG

FIGURE 132

MVPAWLWLLCVSVPQALPKAQP AELSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSG
KATEGPFAMDPDSGFLLVTRALDREEQA EYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVP
HFSQAIYRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQPS PDMFQLEPRL
GALALSPKGSTSLDHALERTYQLLVQVKMDGDQASGHQATATVEVSI IESTWVSLEPIHLAE
NLKVLYPHHMAQVHWSGGDVHYHLESHPPGPF EVNAEGNLYVTRELDREAQA EYLLQVRAQN
SHGEDYAAPLELHVLVMDENDNVPICPPRDPTVSIPELSPPGTEVTRL SAEDADAPGSPNSH
VVYQLLSPEPEDGVEGRAFQVDPTSGSVTLGVLPLRAGQNILLVLAMDLAGAEGGFSSTCE
VEVAVTDINDHAPEFITSQIGPISLPEDVEPGTLVAMLTADADLEPAFRLMDFAIERGDTE
GTFGLDWEPD SGHVRLRLCKNLSYEAAPSHEVVVVVQSVAKLVGPGPGPGATATVTVLVERV
MPPPKLDQESYEASVPISAPAGSFL LTIQPSDPISRTLRFSLVNDSEGWLCIEKFSGEVHTA
QSLQGAQPGDTYTVLVEAQDTALT LAPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF
TLGPNPTVQRDWRLQTLNGSHAYLTLALHWVEPREHIIPVVVSHNAQMWQLLVRVIVCRCNV
EGQCMRKVGRMKGMPTKLSAVGILVGT LVAIGIFLILIFTHWTMSRKKDPDQPADSVPLKATV

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 762-784

CCGGGGAC**ATG**AGGTGGGATACTGTTTCATTGGGGCCCTTATTGGGTCCAGCATCTGTGGCCAA
GAAAAATTTTTTGGGGACCAAGTTTTTGAGGATTAATGTCAGAAATGGAGACGAGATCAGCAA
ATTGAGTCAACTAGTGAATTCAAACAACCTGAAGCTCAATTTCTGGAAATCTCCCTCCTCCT
TCAATCGGCCTGTGGATGTCCTGGTCCCATCTGTCTAGTCTGCAGGCATTTAAATCCTTCCTG
AGATCCCAGGGCTTAGAGTACGCAGTGACAATTGAGGACCTGCAGGCCCTTTTAGACAATGA
AGATGATGAAATGCAACACAATGAAGGGCAAGAACGGAGCAGTAATAACTTCAACTACGGGG
CTTACCATTCCCTGGAAGCTATTTACCACGAGATGGACAACATTGCCGCAGACTTTTCCTGAC
CTGGCGAGGAGGGTGAAGATTGGACATTCGTTTTGAAAACCGGCCGATGTATGTACTGAAGTT
CAGCACTGGGAAAGGCGTGAGGCGGCCGGCCGTTTGGCTGAATGCAGGCATCCATTCCCAGAG
AGTGGATCTCCCAGGCCACTGCAATCTGGACGGCAAGGAAGATTGTATCTGATTACCAGAGG
GATCCAGCTATCACCTCCATCTTGAGAGAAAATGGATATTTTTCTTGTTGCCTGTGGCCAATCC
TGATGGATATGTGTATACTCAAACCTCAAACCGATTATGGAGGAAGACGCGGTCCCGAAATC
CTGGAAGCTCCTGCATTGGTGCTGACCCAAATAGAACTGGAACGCTAGTTTTTGACAGGAAAG
GGAGCCAGCGACAACCCTTGCTCCGAAGTGTACCATGGACCCACGCCAATTCCGAAGTGGAG
GGTGAAATCAGTGGTAGATTTTCATCCAAAACATGGGAATTTCAAGGGCTTCATCGACCTGC
ACAGCTACTCGCAGCTGCTGATGTATCCATATGGGTACTCAGTCAAAAAGGCCCCAGATGCC
GAGGAACCTGCACAAGGTGGCGAGGCTTGCGGCCAAAGCTCTGGCTTCTGTGTCGGGGACTGA
GTACCAAGTGGGTCCCACCTGCACCACTGTCTATCCAGCTAGCGGGAGCAGCATCGACTGGG
CGTATGACAACGGCATCAAATTTGCATTACATTTGAGTTGAGAGATACCGGGACCTATGGC
TTCCTCCTGCCAGCTAACCAGATCATCCCCACTGCAGAGGAGACGTGGCTGGGGCTGAAGAC
CATCATGGAGCATGTGCGGGACAACCTCTAC**TAG**GGCGATGGCTCTGCTCTGTCTACATTTAT
TTGTACCCACACGTGCACGCACTGAGGCCATTGTTAAAGGAGCTCTTTCCTACCTGTGTGAG
TCAGAGCCCTCTGGGTTTGTGGAGCACACAGGCCTGCCCTCTCCAGCCAGCTCCCTGGAGT
CGTGTGTCTCTGGCGGTGTCCCTGCAAGAACTGGTCTGCCAGCCTGCTCAATTTTGGTCTCTG
CTGTTTTTGTATGAGCCTTTTGTCTGTTTCTCCTTCCACCCTGCTGGCTGGGCGGCTGCACTC
AGCATCACCCCTTCCTGGGTGGCATGTCTCTCTCTACCTCATTTTTTAGAACCAAAGAACATC
TGAGATGATTCTCTACCCCTCATCCACATCTAGCCAAGCCAGTGACCTTGCTCTGGTGGCACT
GTGGGAGACACCACTTGTCTTTAGGTGGGTCTCAAAGATGATGTAGAATTTCTTTAATTTTC
TCGCAGTCTTCCTGGAAAATATTTTTCTTTTGGAGCAGCAAATCTTGTTAGGGATATCAGTGAAG
GTCTCTCCCTCCCTCCTCTCCTGTTTTTTTTTTTTTTTTTGGAGACAGAGTTTTGCTCTTGTTGCC
CAGGCTGGAGTGTGATGGCTCGATCTTGGCTCACCAACAACCTCTGCCTCCTGGGTTCAAGCA
ATTCTCCTGCCTCAGCCTCTTGAGTAGCTTGGTTTATAGGCGCATGCCACCATGCCTGGCTA
ATTTTGTGTTTTTTAGTAGAGACAGGGTTTCTCCATGTTGGTCAGGCTGGTCTCAAACCTCCCA
ACCTCAGGTGATCTGCCCTCCTTGGCCTCCCAGAGTGCTGGGATTACAGGTGTGAGCCACTG
TGCCGGGGCCCGTCCCCTCCTTTTTTTAGGCCTGAATACAAAGTAGAAGATCACTTTCCTTCAC
TGTGCTGAGAATTTCTAGATACTACAGTTCTTACTCCTCTCTTCCCTTTGTTATTCAGTGTG
ACCAGGATGGCGGGAGGGGATCTGTGTCACTGTAGGTACTGTGCCCAGGAAGGCTGGGTGAA
GTGACCATCTAAATTGCAGGATGGTGAAATTATCCCCATCTGTCCTAATGGGCTTACCTCCT
CTTTGCCTTTTGAACCTCACTTCAAAGATCTAGGCCTCATCTTACAGGTCCTAAATCACTCAT
CTGGCCTGGATAATCTCACTGCCCTGGCACATTCCCATTTGTGCTGTGGTGTATCCTGTGTT
TCCTTGTCCTGGTTTG
TCTGTCTATTTTGTATCCTGGACCACAAGTTCCTAAGTAGAGCAAGAATTCATCAACCAGCT
GCCTCTTGTTTCATTTACCTCAGCACGTACCATCTGTCCTTTTGTGTTGTGTGTGTGTGTGTG
TTGTTTTTTTTGCTTTTACCAAACATGTCTGTAAATCTTAACCTCCTGCCTAGGATTTGTACA
GCATCTGGTGTGTGCTTATAAGCCAATAAATATTCAATGTGAAAAAAAAAAAAAAAAAAAA

FIGURE 134

MRWILFIGALIGSSICGQEKFFGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFNR
PVDVLVPSVSLQAFKSFLRSQGLEAYVTIEDLQALLDNEDDEMQHNEGQERSNNFNYGAYH
SLEAIYHEMDNIAADFPDLARRVKIGHSFENRPMYVLKFSTGKGVRRPAVWLNAGIHSREWI
SQATAIWTARKIVSDYQRDPAITSILEKMDIFLLPVANPDGYVYTQTQNRLWRKTRSRNPGS
SCIGADPNRNWNASFAGKGASDNPCSEVYHGPHANSEVEVKSVDIFIQKHGNFKGFIDLHSY
SQLLMYPYGYSVKKAPDAEELDKVARLAAKALASVSGTEYQVGPTCTTVYPASGSSIDWAYD
NGIKFAFTFELRDTGTYGFLLPANQIIPTAEETWLGLKTIMEHVVDONLY

Signal peptide:

amino acids 1-16

135/249

FIGURE 135

[illegible]

FIGURE 136

MASYLYGVLFVAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLE
TPSQNIFFSPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESAIHQGFQHLVHSLTVP
SKDLTLKMGSALFVKKELQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQ GK
VVDIIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMMHQKEQFAF
GVDTELNCFVLQMDYKGDVAFAFVLPSKGKMRQLEQALSARTLIKWSHSLQKRWIEVFIPRF
SISASYNLETILPKMGIQNAFDKNADESGIAKRDSLQVSKATHKAVLDVSEEGTEATAATTT
KFIVRSKDGPSYFTVSEFNRTFLMMITNKATDGILFLGKVENPTKS

Signal peptide:

amino acids 1-20

137/249

[illegible]

FIGURE 138

MKMQKGNVLLMFGLLLHLEAATNSNETSTTSANTGSSVISSGASTATNSGSSVTSSGVSTATI
SGSSVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSE
SSTPSSGASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSS
TTSSGASTATNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTT
SNGAGTATNSESSTTSSGASTATNSDSSTVSSGASTATNSESSTTSSGASTATNSESSTSS
GASTATNSDSSTTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGA
NTATNSESSTVSSGASTATNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSTTSSEAST
ATNSESSTVSSGISTVTNSESSTTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAV
SEAKPGGSLVPWEIFLITLVSVVAAVGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGP
GPGGNHGAPHRPRWSPNWFWRPVS SIAMEMSGRNSGP

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

FIGURE 139

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTC
CCAGCAAT**ATG**CATCTTGCACGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCC
CTGTCTGGATGGGCGGCCAGCGATGACCCCATTGAGAAGGTCATTGAAGGGATCAACCGAGG
GCTGAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGGAATCACGC
ATGCCGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGC
AAGGAGTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGAT
CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACG
CTGCTGGACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGGTCCAC
CAGGCTGGGAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGG
AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCACCATGCTGCTGGCCAGGCCGGGAAGGAGC
TGCAGAATGCTCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGC
AACCATCAAAGCGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGG
GGCCTCAGTCAACACGCCTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCA
TGCCCT**TAA**ACTGGCATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTCACATCAGCTGAC
ATGACCTGGAGGGGTTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGGTTGTACTG
GGATTTGTGAATAAACTTGATACACCA

FIGURE 140

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675

><subunit 1 of 1, 247 aa, 1 stop

><MW: 25335, pI: 7.00, NX(S/T): 0

MHLARLVGSCSLLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAG
REVEKVFNGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAG
QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQN
AHNGVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP

Important features of the protein:**Signal peptide:**

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

141/249

FIGURE 141

CTCGGGGTCCCCAGGGGGCTGCGCCGGGGCCGGCCTGGCAAGGGGGACGAGTCAGTGGACACTCCAGGAAGAGCGGC
 CCGCGGGGGGGCGATGACCGTGCGCTGACCGTGACTCACTCCAGGTCCGGAGGCGGGGGCCCCGGGGCGACTCG
 GGGGCGGACCGCGGGGGCGGAGCTGCCGCCCGTGAGTCCGGCCGAGCCACCTGAGCCCGAGCCGCGGGACACCGTC
 GCTCCTGCTCTCCGAATGCTGCGCACCGCGATGGGCCTGAGGAGCTGGCTCGCCGCCCATGGGGCGCGCTGCCG
 CCTCGGCCACCGCTGCTGCTGCTCCTGCTGCTGCTGCTCCTGCTGCAGCCGCCGCTCCGACCTGGGCGCTCAGC
 CCCCAGATCAGCCTGCCCTCTGGGCTCTGAAGAGCGGCCATTCTCAGATTGGAAGCTGAACACATCTCCAACCTAC
 ACAGCCCTTCTGCTGAGCAGGGATGGCAGGACCGTGTACGTGGGTGCTCGAGAGGCCCTCTTTGCACTCAGTAGC
 AACCTCAGCTTCCCTGCCAGGCGGGGAGTACCAGGAGCTGCTTTGGGGTGACAGACGCAGAGAAGAAACAGCAGTGC
 AGCTTCAAGGGCAAGGACCCACAGCGCAGCTGTCAAACTACATCAAGATCCTCCTGCCGCTCAGCGGCAGTCAC
 CTGTTACCTGTGGCACAGCAGCCTTACGCCCCATGTGTACCTACATCAACATGGAGAAGCTTACCCTGGCAAGG
 GACGAGAAGGGGAATGTCTCCTGGAAGATGGCAAGGGCCGTTGTCCCTTCGACCCGAATTTCAAGTCCACTGCC
 CTGGTGGTTGATGGCGAGCTCTACACTGGAACAGTCAGCAGCTTCCAAGGGGAATGACCCGGCCATCTCGCGGAGC
 CAAAGCCTTCGCCCCACCAAGACCGAGAGCTCCCTCAACTGGCTGCAAGACCCAGCTTTTGTGGCCTCAGCCTAC
 ATTCTGAGAGCCTGGGCAGCTTGCAAGGCGATGATGACAAGATCTACTTTTCTTCAGCGAGACTGGCCAGGAA
 TTTGAGTTCTTTGAGAACACCATTTGTGTCCCGCATTTGCCGCATCTGCAAGGGCGATGAGGGTGAGAGCGGGTG
 CTACAGCAGCGCTGGACCTCCTTCCCAAGGCCAGCTGCTGTGCTCACGGCCCCGACGATGGCTTCCCCTTCAAC
 GTGCTGCAGGATGTCTTCACGCTGAGCCCCAGCCCCAGGACTGGCGTGACACCCCTTTTCTATGGGGTCTTCACT
 TCCCAGTGGCACAGGGGAACACAGAAGGCTCTGCCGTCTGTGTCTTCAACAATGAAGGATGTGCAGAGAGTCTTC
 AGCGGCCTCTACAAGGAGGTGAACCGTGAGACACAGCAGTGGTACACCGTGACCCACCCGGTGCCACACCCCGG
 CCTGGAGCGTGCATCACCAACAGTGCCCGGGAAGGAAGATCAACTCATCCCTGCAGCTCCACAGCCGCTGCTG
 AACTTCTCAAGGACCACCTTCTGATGGACGGGCAGGTCCGAAGCCGATGCTGCTGCTGCAGCCCCAGGCTCGC
 TACCAGCGCTGGCTGTACACCGCTCCCTGGCCTGCACCACACCTACGATGTCTCTTCTGGGCACTGGTGAC
 GGCCGGCTCCACAAGGCAGTGAGCGTGGGCCCCGGGTGCACATCATTGAGGAGCTGCAGATCTTCTCATCGGGA
 CAGCCCGTGCAAGATCTGCTCCTGGACACCCACAGGGGCTGCTGTATGCGGCCTCACACTCGGGCGTAGTCCAG
 GTGCCCATGGCCAACTGCAGCCTGTACCGGAGCTGTGGGACTGCCTCCTCGCCGGGACCCCTACTGTGCTTGG
 AGCGGCTCCAGCTGCAAGCACGTGAGCCTTACCAGCCTCAGCTGGCCACCAAGGCCGTGGATCCAGGACATCGAG
 GGAGCCAGCGCCAAGGACCTTTGCAGCGCTCTTCGGTTGTGTCCCGCTCTTTGTACCAACAGGGGAGAAGCCA
 TGTGAGCAAGTCCAGTTCAGCCCAACACAGTGAACACTTTGGCCTGCCCGCTCCTCTCCAACCTGGCGACCCGA
 CTCTGGCTACGCAACGGGGCCCCCGTCAATGCCCTCGGCCTCCTGCCACGTGCTACCCACTGGGGACCTGCTGCTG
 GTGGGCACCCAAACAGCTGGGGGAGTTCCAGTGTGGTCACTAGAGGAGGGCTTCCAGCAGCTGGTAGCCAGCTAC
 TGCCAGAGGTGGTGGAGGACGGGTGGCAGACCAACAGATGAGGGTGGCAGTGTACCCGTATTATCAGCACA
 TCGCGTGTGAGTGACCAAGCTGGTGGCAAGGCCAGCTGGGGTGACAGACAGTCTTACTGGAAGGAGTTCTGCTG
 ATGTGCACGCTCTTTGTGCTGGCCGTGCTGCTCCAGTTTTATTCTTGTCTTACCGGCACCGGAACAGCATGAAA
 GTCTTCTGAAGCAGGGGGAATGTGCCAGCGTGACCCCAAGACCTGCCCTGTGGTGTGCCCCCTGAGACCCGC
 CCACTCAACGGCCTAGGGCCCCCTAGCACCCCGTCCGATACCGAGGGTACCAGTCCCTGTGAGACAGCCCCCG
 GGGGCCCCGAGTCTTCACTGAGTCAGAGAAGAGGCCACTCAGCATCCAAGACAGCTTCGTGGAGGTATCCCCAGTG
 TGCCCCCGGGCCCCGGGTCCGCTTGGCTCGGAGATCCGTGACTCTGTGGTGTGAGAGCTGACTTCCAGAGGACGC
 TGCCCTGGCTTCAGGGGCTGTGAATGCTCGGAGAGGGTCAACTGGACCTCCCTCCGCTCTGCTCTTCTGTTGAAC
 ACGACCGTGGTGCCCGGCCCTTGGGAGCCTTGGAGCCAGCTGGCCTGCTGCTCTCCAGTCAAGTAGCGAAGCTCC
 TACCACCCAGACACCCAAACAGCCGTGGCCCCAGAGGTCTGGCCAAATATGGGGGCTGCCTAGGTTGGTGGAA
 CAGTGTCTCTTATGTAACTGAGCCCTTTGTTTTAAAAACAATTCCAAATGTGAAACTAGAATGAGAGGGAAGAG
 ATAGCATGGCATGCAGCACACAGGCTGCTCCAGTTTATGGCCTCCAGGGGTGCTGGGGATGCATCCAAAGTGG
 TTGTCTGAGACAGAGTTGGAACCCCTACCAACTGGCCTCTTCACTTCCACATTATCCCGCTGCCACCGGCTGC
 CCTGTCTCACTGCAGATTACGAGACAGCTTGGGCTGCGTGCGTTCTGCCTTGCCAGTCAGCCGAGGATGTAGTTG
 TTGCTGCCGTGCTCCACACCTCAGGGACCAGAGGGCTAGGTTGGCACTGCGGCCCTCACCAGGTCTGGGCTC
 GGACCCAACTCCTGGACCTTTCCAGCCTGTATCAGGCTGTGGCCACACGAGAGGACAGCGGAGCTCAGGAGAGA
 TTTCTGTGACAATGTACGCCCTTCCCTCAGAATTCAGGGAAGAGACTGTGCGCTGCCTTCTCCGTTGTTGCGTGA
 GAACCCGTGTGCCCCCTTCCACCATATCCACCTCGCTCCATCTTTGAACTCAAACACGAGGAAGTAACTGCACC
 CTGGTCTCTCCCGAGTCCCGAGTTCACCTCCATCCCTCACCTTCTTCACTCTAAGGGATATCAACACTGCCC
 AGCACAGGGGCCCTGAATTTATGTGGTTTATATACATTTTTTAATAAGATGCACCTTTATGTATTCTTTAATAAA
 GTCTGAAGAATTACTGTTTTAAAAA

FIGURE 142

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962

><subunit 1 of 1, 837 aa, 1 stop

><MW: 92750, pI: 7.04, NX(S/T): 6

MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLLLLLQPPPPTWALSPRISLPLGSEERPFLRF
EAEHISNYTALLLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELLWGADAEKKQQCSFKG
KDPQRDCQNYIKILLPLSGSHLFTCGTAAAFSPMCTYINMENFTLARDEKGNVLLEDGKGRCP
FDPNFKSTALVVDGELYTGTVSSFQGNDAISRSQSLRPTKTESSLNWLQDPAFVASAYIPE
SLGSLQGDDDKIYFFFSETGQEFFEFFENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLC
SRPDDGFPPFENVLQDVFTLSPSPQDWRDTLFYGVFTSQWHRGTTEGSAVCVFTMKDVQRVFSG
LYKEVNRETQQWYTVTHPVPTPRPGACITNSARERKINSSQLPDRVLNFLKDHFLMDGQVR
SRMLLLQPQARYQRVAVHRVPGLHHTYDVLFLGTGDGRLHKAVSVGPRVHIIIEELQIFSSGQ
PVQNLLLDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSLEYQP
QLATRPWIQDIEGASAKDLCSASSVVSPSFVPTGEKPCEQVQFQPNVTNLTACPLLSNLATR
LWLRNGAPVNASASCHVLPTGDLLLVGTTQQLGEFQCWSLEEGFQQLVASYCPEVVEDGVADQ
TDEGGSVPVIIISTSRVSAPAGGKASWGADRSYWKEFLVMCTLFVLAVLLPVLFLLYRHRNSM
KVFLKQGECA SVHPKTCPVVLPPEPTRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFTSEKR
PLSIQDSFVEVSPVCPRPRVRLGSEIRDSVV

Transmembrane domains:

amino acids 23-46 (type II), 718-738

FIGURE 143A

CTAAGCCGGAGGATGTGCAGCTGCGGCGGCGGCGCCGGCTACGAAGAGGACGGGGACAGGCGCCGTGCGAACCGA
 GCCCAGCCAGCCGAGGACGCGGGCAGGGCGGGACGGGAGCCCGGACTCGTCTGCCGCCGCCGTCTGCGCGTGC
 TGCCGGCCCCCGCTCCCCGCGCGGAGCGGGAGGAGCCGCCACCTCGCGCCGAGCCGCCGCTAGCGCGCGC
 CGGGCATGGTCCCCTCTTAAAGGCGCAGGCCGCGGCGGGGGCGGGTGTGCGGAACAAAGCGCCGGCGCGGGG
 CCTGCGGGCGGCTCGGGGGCCGCGATGGGCGCGGCGGGCCCCGCGGCGGCGGCGGCGCTGCCCGGGCCGGGCTCG
 CGGCGCTAGGGCGGGCTGGCCTCCGTGGGCGGGGGCAGCGGGCTGAGGGCGCGCGGAGCCTGCGGCGGCGGGCGG
 GGCGGCGGCGGCGGCCCGGCGGGCGGAGCGGCGCGGGC**ATG**GCGCGCGCGGCGGCGGCGGCGCTGGCTCAGCGTGC
 TGCTCGGGCTCGTCTGGGCTTCGTGCTGGCCTCGCGGCTCGTCTGCCCGGGCTTCCGAGCTGAAGCGAGCGG
 GCCCACGGCGCCGCGCCAGCCCCGAGGGCTGCCGGTCCGGGCAGGCGGCGGCTTCCAGGCCGGCGGGGCGCGCG
 GCGATGCGCGCGGGGCGCAGCTCTGGCCGCCCGGCTCGGACCCAGATGGCGGCCCCGCGCGACAGGAACCTTTCTCT
 TCGTGGGAGTCAATGACCGCCAGAAATACCTGCAGACTCGGGCCGTGGCCGCTACAGAACATGGTCCAAGACAA
 TTCTTGGGAAAGTTCACTTCTTCTCAAGTGAGGGTTCTGACACATCTGTACCAATTCAGTAGTGCCACTACGGG
 GTGTGGACGACTCCTACCCGCCCCAGAAAGTCTTTCATGATGCTCAAGTACATGCACGACCACTACTTGGACA
 AGTATGAATGGTTTATGAGAGCAGATGATGACGTGTACATCAAAGGAGACCGTCTGGAGAAGTTCTGAGGAGTT
 TGAACAGCAGCGAGCCCCCTCTTCTTGGGCGACAGGCGCTGGGCACACGGAAGAAATGGGAAAAGTTGGCCCTGG
 AGCCTGGTGAGAACTTCTGCATGGGGGGGCTGGCGTGATCATGAGCCGGGAGGTGCTTGGGAGAATGGTGCCGC
 ACATTGGCAAGTGTCTCCGGGAGATGTACACCACCCATGAGGACGTGGAGGTGGGAAGGTGTGTCCGGAGGTTTG
 CAGGGGTGCACTGTGTCTGGTCTTATGAGATGCGGCAGCTTTTTTATGAGAATTACGAGCAGAACAAAAAGGGGT
 ACATTAGAGATCTCCATAACAGTAAAAATTCACCAAGCTATCACATTACACCCCAACAAAAACCCACCCTACCAGT
 ACAGGCTCCACAGCTACATGCTGAGCCGCAAGATATCCGAGCTCCGCCATCGCACAAATACAGCTGCACCGCGAAA
 TTGTCCTGATGAGCAAATACAGCAACACAGAAATTCATAAAGAGGACCTCCAGCTGGGAATCCCTCCCTCCTTCA
 TGAGGTTTTCAGCCCCGCCAGCGAGAGGAGATTCTGGAATGGGAGTTTCTGACTGGAAAATACTTGTATTGCGCAG
 TTGACGGCCAGCCCCCTCGAAGAGGAATGGACTCCGCCAGAGGGAAGCCTTGGACGACATTGTTCATGCAGGTCA
 TGGAGATGATCAATGCCAACGCCAAGACCAGAGGGCGCATCATTGACTTCAAAGAGATCCAGTACGGCTACCGCC
 GGGTGAACCCCATGTATGGGGCTGAGTACATCCTGGACCTGCTGCTTCTGTACAAAAGCACAAAGGGAAGAAAA
 TGACGGTCCCTGTGAGGAGGCACGCGTATTTACAGCAGACTTTCAGCAAAATCCAGTTTGTGGAGCATGAGGAGC
 TGGATGCACAAGAGTTGGCCAAGAGAATCAATCAGGAATCTGGATCCTTGTCTTTCTCTCAAATCCCTGAAGA
 AGCTCGTCCCCCTTTCAGTCCCTGGGTGCAAGAGTGAGCACAAAGAACCCAAAGATAAAAAGATAAACATACTGA
 TTCTTTTGTCTGGGCGTTTCGACATGTTTGTGAGATTTATGGGAACTTTGAGAAGACGTGTCTTATCCCCAATC
 AGAACGTCAAGCTCGTGGTTCTGCTTTTCAATTCTGACTCCAACCTGACAAGGCCAAACAAGTTGAAGTATGA
 GAGATTACCGCATTAAGTACCCTAAGCCGACATGCAGATTTTGCTGTGTCTGGAGAGTTTTCAGAGCCCTGG
 CCTGGAAAGTAGGATCCTCCCACTTTAACAATGAATCTTTGCTCTTCTTCTGCGACGTGACCTCGTGTTTACTA
 CAGAATTCCTTCAGCGATGTCGAGCAAATACAGTTCTGGGCCAACAAATATATTTTCCAATCATCTTCAGCCAGT
 ATGACCCAAAGATTGTTTATAGTGGGAAAGTTCCAGTGACAACCATTTTGCCTTTACTCAGAAAAGTTGGCTTCT
 GGAGAACTATGGGTTTGGCATCACCTGTATTTATAAGGGAGATCTTGTCCGAGTGGGTGGCTTTGATGTTTCCA
 TCCAAGGCTGGGGGCTGGAGGATGTGGACCTTTTCAACAAGGTTGTCCAGGCAGGTTTGAAGACGTTTAGGAGCC
 AGGAAGTAGGAGTAGTCCACGTCCACCATCCTGTCTTTTGTGATCCCAATCTTGACCCAAACAGTACAAAATGT
 GCTTGGGTCCTAAAGCATCGACCTATGGGTCCACCCAGCAGCTGGCTGAGATGTGGCTGGAAAAAATGATCCAA
 GTTACAGTAAAAGCAGCAATAAATAATGGCTCAGTGAGGACAGCC**TAA**TGTCCAGCTTTGCTGGAAAAGACGTTTT
 TAATTATCTAATTTATTTTTCAAAAATTTTTTGTATGATCAGTTTTTGAAGTCCGTATACAAGGATATATTTTAC
 AAGTGGTTTTCTTACATAGGACTCCTTTAAGATTGAGCTTTCTGAACAAGAAGGTGATCAGTGTGTGCTTTGAA
 CACATCTTCTTGTGAACATTATGTAGCAGACCTGCTTAACTTTGACTTGAATGTACCTGATGAACAAAAGTTT
 TTTAAAAAATGTTTTCTTTTGAACCTTTGCTCCAGTCTATGGCAGAAAACGTGAACATTCTGCAAGATTA
 TATTGTAACAAAACACTGTAACCTCTGGTAAATGTTCTGTTGTGATTGTTAACATTCCACAGATTCTACCTTTGT
 GTTTTGTTTTTTTTTTTTACAAATTGTTTTAAAGCCATTTTCATGTTCCAGTTGTAAGATAAGGAAATGTGATAATA
 GCTGTTTCATCATTGTCTTCAGGAGAGCTTTCAGAGTTGATCATTTCTCTCATGGTACTCTGCTCAGCATGGC
 CACGTAGGTTTTTTGTTTGTGTTTTGTTTCTTTTTTGGAGACGGAGTCTCACTCTGTTACCCAGGCTGGAATG
 CAGTGGCGCAATCTTGGCTCACTTTAACCTCCACTTCCCTGGTTCAAGCAATTCCCCTGCCTTTGCCTCCCGAGT
 AGCTGGGATTACAGGCACACACCACCGCCAGNATAGTTTTTTTGTATTTTGTAGTAGAGACGGGTTTACCAT
 GCAAGCCCAGCTGGCCACGTAGGTTTTTAAAGCAAGGGGCGTGAAGAAGGCACAGTGAGGTATGTGGCTGTTCTCG
 TGGTAGTTTATTGCGCCTAAATAGACCTGGCATTAAATTTCAAGAAGGATTTGGCATTCTCTCTTGTGACCCTT
 CTCTTTAAAGGGTAAAATATTAATGTTTAGAATGACAAAGATGAATTATTACAATAAATCTGATGTACACAGACT
 GAAACATACACACATACCCCTAATCAAAACGTTGGGGAAAAATGTATTTGGTTTTGTTTCTTTTCATCCTGTCTG
 TGTATGTGGGTGGAGATGGTTTTTCATTCTTTCACTACTGTTTTGTTTTATCCTTTGTATCTGAAATACCTTTAA
 TTTATTTAATATCTGTGTTTCAGAGCTCTGCCATTTCTTGAGTACCTGTTAGTTAGTATTATTTATGTGTATCGG
 GAGTGTGTTTAGTCTGTTTTATTTGCAGTAAACCGATCTCCAAAGATTTCTTTTGGAAACGCTTTTTCCCTCC

144/249

FIGURE 143B

TTAATTTTATATTCCTTACTGTTTTACTAAATATTAAGTGTTCTTTGACAATTTTGGTGCTCATGTGTTTTGGG
GACAAAAGTGAAATGAATCTGTCATTATACCAGAAAAGTTAAATTCTCAGATCAAATGTGCCTTAATAAATTTGTT
TTCATTTAGATTTCAAACAGTGATAGACTTGCCATTTTAATACACGTCATTGGAGGGCTGCGTATTTGTAAATAG
CCTGATGCTCATTTGGAAAAATAAACAGTGAACAATATTTTCTATTGTACTTTTGAACCATTTTGTCTCATT
ATTCCTGTTTTAGCTGAAGAATTGTATTACATTTGGAGAGTAAAAAAGTTAAACACGAAAAAA

145/249

FIGURE 144

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836

><subunit 1 of 1, 802 aa, 1 stop

><MW: 91812, pI: 9.52, NX(S/T): 3

MAARGRRRAWLSVLLGLVLGFLVLA SRLVLPRA SELKRAGPRRRASPEGCRSGQAAASQAGGAR
GDARGAQLWPPGSDPDGGPRDRNFLFVGVM TAQKYLQTRAVAAYRTWSKTIPGKVQFFSSEG
SDTSVPIPVVPLRGVDDSYPPQKKSFMM LKYMHDHYLDKYEFWMRADDVYIKGDRL ENFLR
SLNSSEPLFLGQTGLGTTEEMGKLAL EPGENFCMGGPGVIMSREVLRRMVP HIGKCLREMYT
THEDVEVGRCVRRFAGVQC VWSYEMRQLFYENYEQNKKGYIRDLHNSKI HQAITLHPNKNPP
YQYRLHSYMLSRKISELRHRTIQLHREIV LMSKYSNTEIHKEDLQLGIPPSFMR FQPRQREE
ILEWEFLTGKYLYSAVDGQPPRRGMDSAQ REALDDIVMQVMEMINANAKTRGRIIDFKEIQY
GYRRVNP MYGAEYILDLLLLYKKHKGKKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKR
INQESGSL SFLSNSLKKLVFPQLPGSKSEHK EKPDKKINILIPLSGRFDMFVRFMGNFEKTC
LIPNQNVKLVLLFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQ
FNNESLLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSDNHFAFT
QKTGFWRNYGFGITCIYKGD LVRVGGFDVSIQGWGLEDVDLFNKVVQAGLKTFRSQEVGVVH
VHHPVFCDPNLDPKQYKMCLGSKASTYGSTQQ LAEMWLEKNDPSYSKSSNNNGSVRTA

Signal peptide:

amino acids 1-23

FIGURE 145

GGACAACCGTTGCTGGGTGTCCCAGGGCCTGAGGCAGGACGGTACTCCGCTGACACCTTCCC
TTTCGGCCTTGAGGTTCCCAGCCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGCT
ACGGACGACGCCT**ATGA**AAGCCCTTAGTCCTTCTAGTTGCGCTTTTGCTATGGCCTTCGTCTG
TGCCGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAACTTGAATCATTATATA
CAAGTTTTAGAGAACCTAGTACGAAGTGTTCCCTCTGGGGAGCCAGGTCGTGAGAAAAATC
TAACTCTCCAAACATGTTTATTCTATAGCATCAAAGGGATCAAAATTTAAGGAGCTAGTTA
CACATGGAGACGCTTCAACTGAGAATGATGTTTTAACCAATCCTATCAGTGAAGAACTACA
ACTTTCCTACAGGAGGCTTCACACCGGAAATAGGAAAGAAAAACACACGGAAAGTACCCC
ATTCTGGTCGATCAAACCAAACAATGTTTCCATTGTTTTGCATGCAGAGGAACCTTATATTG
AAAATGAAGAGCCAGAGCCAGAGCCGGAGCCAGCTGCAAAACAACTGAGGCACCAAGAATG
TTGCCAGTTGTTACTGAATCATCTACAAGTCCATATGTTACCTCATAACAAGTCACCTGTCAC
CACTTTAGATAAGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCCCTCAGCTCT
CAGGTGAACTGCGATAGAAAAACCCGAAGAGTTTGGAAGCACCCAGAGAGTTGGAATAAT
GATGACATTTTGAAAAAAATTTTAGATATTAATTCACAAGTGCAACAGGCACTTCTTAGTGA
CACCAGCAACCCAGCATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAAACGAAGCC
TTGCTCTAGCAGCAGCAGCAGAACATAAATTA AAAACAATGTATAAGTCCCAGTTATTGCCA
GTAGGACGAACAAGTAATAAAATTGATGACATCGAACTGTTATTAACATGCTGTGTAATTC
TAGATCTAACTCTATGAATATTTAGATATTAATGTGTTCCACCAGAGATGAGAGAAAAAG
CTGCTACAGTATTCAATACATTAAAAAATATGTGTAGATCAAGGAGAGTCACAGCCTTATTA
AAAGTTTAT**TAA**ACAATAATATAAAAAATTTTAAACCTACTTGATATTCCATAACAAAGCTGA
TTTAAGCAAACCTGCATTTTTTTCACAGGAGAAATAATCATATTCGTAATTTCAAAAGTTGTAT
AAAAATATTTTCTATTGTAGTTCAAATGTGCCAACATCTTTATGTGTCATGTGTTATGAACA
ATTTTCATATGCACTAAAAACCTAATTTAAATAAAATTTTGGTTCAGGAAAAA

FIGURE 146

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864

><subunit 1 of 1, 350 aa, 1 stop

><MW: 39003, pI: 5.59, NX(S/T): 1

MKPLVLLVALLLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRVPSGEPGREKKSNSPK
HVYSIASKGSKFKELVTHGDASTENDVLTNPIS ETTTFPTGGFTPEIGKKKHTESTPFWSI
KPNNVSIVLHAEEPYIENEEPEPEPEPAAKQTEAPRMLPVVTESSTSPYVTSYKSPVTTLDK
STGIEISTESEDVPQLSGETAIEKPEEFGKHPESWNNDILKKILDINSQVQQALLSDTSNP
AYREDIEASKDHLKRSLALAAAAEHKLKTMYSQLLPVGRTSNKIDDIETVINMLCNSRSKL
YEYLDIKCVPPEMREKAATVFNTLKNMCRSRRVTALLKVY

Signal peptide:

amino acids 1-19

148/249

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTG
ACCTCCAAATCATCCATCCACCCCTGCTGTCATCTGTTTTCATAGTGTGAGATCAACCCACA
GGAATATCC**ATG**GCTTTTGTGCTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTCAAGGACA
GTGGCAAGTCACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCT
CCTGCTCCCTCTTTCTGAGACCAGTGCAGAGGCTATGGAAGTGCGGTCTTTCAGGAATCAG
TTCCATGCTGTGGTCCACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACA
GTATCGAGGGAGAACTGAGTTTGTGAAGGACTCCATTGCAGGGGGGCGTGTCTCTCTAAGGC
TAAAAAACATCACTCCCTCGGACATCGGCCTGTATGGGTGCTGGTTCAGTTCCAGATTTTAC
GATGAGGAGGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCCTCTCATTTCCAT
CGTGGGATATGTTGACGGAGGTATCCAGTTACTCTGCCTGTCCTCAGGCTGGTTCCTCCAGC
CCACAGCCAAGTGGAAGGTCCACAAGGACAGGATTTGTCTTCAGACTCCAGAGCAAATGCA
GATGGGTACAGCCTGTATGATGTGGAGATCTCCATTATAGTCCAGGAAAATGCTGGGAGCAT
ATTGTGTTCCATCCACCTTGCTGAGCAGAGTCATGAGGTGGAATCCAAGGTATTGATAGGAG
AGACGTTTTTCCAGCCCTCACCTTGGCGCCTGGCTTCTATTTTACTCGGGTTACTCTGTGGT
GCCCTGTGTGGTGTGTGTCATGGGGATGATAATTGTTTTCTTCAAATCCAAAGGGAAAATCCA
GGCGGAAGTGGACTGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGGAAACACG
CAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTTCTGATCTGAAA
ACTGTAACCCATAGAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAA
GAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGGAC
AAAATGTAGGGTGGTATGTGGGAGTGTGTGCGGGATGACGTAGACAGGGGGAAGAACAAATGTG
ACTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTTGTATTTTCAC
ATTCAATCCCCATTTTATCAGCCTCCCCCCCAGCACCCCTCCTACACGAGTAGGGGTCTTCC
TGGACTATGAGGGTGGGACCATCTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACC
CTGCTGACATGTCAGTTTGAAGGCTTGTTGAGACCCTATATCCAGCATGCGATGTATGACGA
GGAAAAGGGGACTCCCATATTCATATGTCCAGTGTCTTGGGGAT**TCA**GACAGAGAAGACCCTG
CTTAAAGGGCCCCACACCACAGACCCAGACACAGCCAAGGGAGAGTGCTCCCGACAGGTGGC
CCCAGCTTCTCTCCGGAGCCTGCGCACAGAGAGTCACGCCCCCCTCTCCTTTAGGGAGC
TGAGGTTCTTCTGCCCTGAGCCCTGCAGCAGCGGCAGTCACAGCTTCCAGATGAGGGGGGAT
TGGCCTGACCCTGTGGGAGTCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCA
CATTAGGTTTAGTTTGTGAAAACCTCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCC
CAGGCTCCTCATTTGCTAGTCACGGACAGTGATTCTGCCTCACAGGTGAAGATTAAAGAGA
CAACGAATGTGAATCATGCTTGCAGGTTTGAGGGCAGCATGTTTGCTAATGATGTGTTTTTA
TATTATACATTTTCCACCAATAAACTCTGTTTGCTTATTCCACATTAATTTACTTTTCTCTA
TACCAAATCACCCATGGAATAGTTATTGAACACCTGCTTTGTGAGGCTCAAAGAATAAAGAG
GAGGTAGGATTTTTCACTGATTCTATAAGCCAGCATTACCTGATACCAAACCAGGCAAAG
AAAACAGAAGAAGAGGAAGGAAAACCTACAGGTCCATATCCCTCATTAACACAGACACAAAAA
TTCTAAATAAAATTTTAACAAATTAAACTAAACAATATATTTAAAGATGATATATAACTACT
CAGTGTGGTTTGTCCCACAAATGCAGAGTTGGTTTAAATATTTAAATATCAACCAGTGTAATT
CAGCACATTAATAAAGTAAAAAAGAAAACCATAAAAAAAAAAAAAAAAAA

FIGURE 148

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866

><subunit 1 of 1, 466 aa, 1 stop

><MW: 52279, pI: 6.16, NX(S/T): 2

MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHA
VVHLYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFESSQIYDEE
ATWELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGY
SLYDVEISIIIVQENAGSILCSIHAEQSHEVESKVLIGETFFQPSPWRLASILLGLLCGALC
GVVMGMIIIVFFKSKGKIQAELDWRRKHGQAELRDARKHAVEVTLPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFRTRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDRGKNNVTLS
PNNGYWVLRLLTTEHLYFTFNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLLT
CQFEGLLRPYIQHAMYDEEKGTPIFICPVSWG

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

FIGURE 149

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTA
GGAAAAGAGTTTGTGGGAACCTGGGTTATCGGCCCTCGTCATCTTCATATCCCTGATTGTC
CTGGCAGTGTGCATTGGACTCACTGTTCAATTATGTGAGATATAATCAAAAGAAGACCTACAA
TTACTATAGCACATTGTCATTTACAACCTGACAACTATATGCTGAGTTTGGCAGAGAGGGCTT
CTAACAATTTTACAGAAATGAGCCAGAGACTTGAATCAATGGTGAAAAATGCATTTTATAAA
TCTCCATTAAGGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTCAGTCAACAGAAGCATGG
AGTGTGGCTCATATGCTGTTGATTTGTAGATTTCACTCTACTGAGGATCCTGAAACTGTAG
ATAAAATTGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTA
GATCCTCACTCAGTTAAAATTAAAAAAATCAACAAGACAGAAACAGACAGCTATCTAAACCA
TTGCTGCGGAACACGAAGAAGTAAACTCTAGGTCAGAGTCTCAGGATCGTTGGTGGGACAG
AAGTAGAAGAGGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGT
GGAGCAACCTTAATTAATGCCACATGGCTTGTGAGTGCTGCTCACTGTTTTACAACATATAA
GAACCCTGCCAGATGGACTGCTTCCTTTGGAGTAACAATAAAACCTTCGAAAATGAAACGGG
GTCTCCGGAGAATAATTGTCCATGAAAATACAAACACCCATCACATGACTATGATATTTCT
CTTGACAGAGCTTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCTCCCTGA
TGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAA
ATGATGGTTACAGTCAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAACT
TGCAATGAACCTCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTT
AGAAGGAAAAACAGATGCATGCCAGGGTGA CTCTGGAGGACCACTGGTTAGTTCAGATGCTA
GAGATATCTGGTACCTTGCTGGAATAGTGAGCTGGGGAGATGAATGTGCGAAACCCAACAAG
CCTGGTGTTTATACTAGAGTTACGGCCTTGCGGGACTGGATTACTTCAAAAACCTGGTATCTATA
AAGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTTGTTTTTTGGGTGTGGAGGCCATT
TTTAGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTTGACTGATCTCAATAAAC
TGTTTGCTTGATGCATGTATTTTCTTCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTG
CCAGATCAACTCTGTCATCTGTGAGCAATAGTTGAAACTTTATGTACATAGAGAAATAGATA
ATACAATATTACATTACAGCCTGTATTCATTTGTTCTCTAGAAGTTTTGTGAGAATTTTGAC
TTGTTGACATAAATTTGTAATGCATATATACAATTTGAAGCACTCCTTTTCTTCAGTTCCTC
AGCTCCTCTCATTTTCAGCAAATATCCATTTTCAAGGTGCAGAACAGGAGTGAAAGAAAATA
TAAGAAGAAAAAAATCCCCTACATTTTATTGGCACAGAAAAGTATTAGGTGTTTTTCTTAGT
GGAATATTAGAAATGATCATATTCATTATGAAAGGTCAAGCAAAGACAGCAGAATACCAATC
ACTTCATCATTTAGGAAGTATGGGAACTAAGTTAAGGAAGTCCAGAAAGAAGCCAAGATATA
TCCTTATTTTTCATTTCCAAACAACTACTATGATAAATGTGAAGAAGATTCTGTTTTTTTTGTG
ACCTATAATAATTATACAACTTCATGCAATGTACTTGTTCTAAGCAAATTAAAGCAAATAT
TTATTTAAACATTGTTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

FIGURE 150

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871

><subunit 1 of 1, 423 aa, 1 stop

><MW: 47696, pI: 8.96, NX(S/T): 3

MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYSTLSFTTD
KLYAEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICR
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTL
GQSLRIVGGTEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFG
VTIKPSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSPVPTYNAVHRVCLPDASYEFQPGDV
MEVTGFGALKNDGYSQNHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGD
SGGPLVSSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

Transmembrane domain:

amino acids 21-40 (type II)

152/249

FIGURE 151

GTCTGAAGGTTATAAAAGCTTCCAGCCAAACGGCATTGAAGTTGAAGATACAACCTGACAGCA
CAGCCTGAGATCTTGGGGATCCCTCAGCCTAACACCCACAGACGTCAGCTGGTGGATTCCCG
CTGCATCAAGGCCTACCCACTGTCTCC**ATG**CTGGGCTCTCCCTGCCTTCTGTGGCTCCTGGC
CGTGACCTTCTTGGTTCCCAGAGCTCAGCCCTTGCCCCCTCAAGACTTTGAAGAAGAGGAGG
CAGATGAGACTGAGACGGCGTGGCCGCCTTTGCCGGCTGTCCCCTGCGACTACGACCACTGC
CGACACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGGTCGGGCGCGGCCTGCCTGTGCCC
AGGACTCTCCAGCCCCGCCCAGCCGCCCCGACCCGCCGCGCATGGGAGAAGTGCGCATTGCGG
CCGAAGAGGGCCGCGCAGTGGTCCACTGGTGTGCCCCCTTCTCCCCGGTCCCTCCACTACTGG
CTGCTGCTTTGGGACGGCAGCGAGGCTGCGCAGAAGGGGGCCCCCGCTGAACGCTACGGTCCG
CAGAGCCGAAGTGAAGGGGCTGAAGCCAGGGGGCATTATATGTCGTTTGCCTAGTGGCCGCTA
ACGAGGCCGGGGCAAGCCGCGTGCCCCAGGCTGGAGGAGAGGGCCTCGAGGGGGCCGACATC
CCTGCCTTCGGGCCTTGACAGCCGCCTTGCGGTGCCGCCCAACCCCCGCACTCTGGTCCACGC
GGCCGTGCGGGTGGGCACGGCCCTGGCCCTGCTAAGCTGTGCCGCCCTGGTGTGGCACTTCT
GCCTGCGCGATCGCTGGGGCTGCCCCGCGCCGAGCCGCCGCCGAGCCGCAGGGGCGCTC**TGA**
AAGGGGCCTGGGGGCATCTCGGGCACAGACAGCCCCACCTGGGGCGCTCAGCCTGGCCCCCG
GGAAAGAGGAAAACCCGCTGCCTCCAGGGAGGGCTGGACGGCGAGCTGGGAGCCAGCCCCAG
GCTCCAGGGCCACGGCGGAGTCATGGTTCTCAGGACTGAGCGCTTGTTTAGGTCCGGTACTT
GGCGCTTTGTTTCCTGGCTGAGGTCTGGGAAGGAATAGAAAGGGGCCCCCAATTTTTTTTAA
AGCGGCCAGATAATAAATAATGTAACCTTTGCGGTTAAAAAAAAAAAAAAAAAAAAA

FIGURE 152

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874

><subunit 1 of 1, 238 aa, 1 stop

><MW: 25262, pI: 6.44, NX(S/T): 1

MLGSPCLLWLLAVTFLVPRAQPLAPQDFEEEEADETETAWPPLPAVPCDYDHCRHLQVPCKE
LQRVGPAACLCPGLSSPAQPPDPPRMGEVRIAAEEGRAVVHWCAFPSPVLHYWLLLWDGSEA
AQKGPPLNATVRRaelKGLKPGGIYVVCVVAANEAGASRVPQAGGEGLEGADIPAFGPCSRL
AVPPNPRTL VHAAVGVGTALALLSCAALVWHFCLRDRWGCPRRAAARAAGAL

Important features of the protein:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 194-220

N-glycosylation site.

amino acids 132-135

AGAGAAAGAAGCGCTCTCCAGCTGAAGCCCAATGCAGGCCCTCCGGCTCTCCGCGAAGAAGTTCC
CTGCCCCGATGAGCCCCCGCGTGCCTCCCCGACTATCCCCAGGCGGGCGTGGGGCACCGGG
CCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGATGGGGC
TTCTCCCTTACGGGGCTCACA**ATG**GCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCTGCT
CTACGCCCTCAATCTGCTCTTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGA
TGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTC
ATTTTGACTTACTTTCTGTGGTTCATCCGGTCATGATTGCTGTTTGTCTGTTTCCTTATCAT
TGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTGCTTCTTGCATGGTACT
TTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAG
GAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTGAAAGCCAGGATGACAAATTA
TGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAATTTTTTTTCAGAGAGAGTTTAAGT
GCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATGACAGAGATGGACTGGCCCCCAGAT
TCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAACAGGCCACCAGGAAGATCTCAGTGA
CCTTTATCAAGAGGGTTGTGGGAAGAAAATGTATTCTTTTTTGAGAGGAACCAACAACACTGC
AGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTCACC
ATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGGACAGACCAATGATGTC
CTTGGAAGAATGACAACCTCTCAGCACCTGTGATGTCCCTCAGTAGAACTGTTGAAACCAAGCC
TGTCAGAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACTTTGAGATGGAG
GAGTTA**TAA**AAAGAAATGTCACAGAAGAAAACCACAACTTGTTTTATTGGACTTGTGAATT
TTTGAGTACATACTATGTGTTTTAGAAATATGTAGAAATAAAAAATGTTGCCATAAAATAACA
CCTAAGCATATACTATTCTATGCTTTAAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCAC
CACCTGGACAATAATTGATGCCCTTAAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGC
CTGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTTGATTAGCATTTT
CGCATCCATGCAAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTT
CTACCAACTAGTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATA
ACTTTTATTACTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTC
AATATTGGTGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAA
GAGCAAGCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAA
TCTGTATAATTTCAGTCGATTTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAA
ATTTGTCCTGTATAGCATCATTATTTTTAGCCTTTCTGTGTTAATAAAGCTTTACTATTCTGT
CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAATTA
CCAGTGTGATACATAGGAATCATTATTGAGAATGATGCTGGCTTTAGGAAGTATTAATAA
GAAAATTTGCACATAACTTAGTTGATTGAGAAAGGACTTGATGCTGTTTTTCTCCCAAATG
AAGACTCTTTTTTGACACTAAACACTTTTTTAAAAAGCTTATCTTTGCTTCTCCAACAAGAA
GCAATAGTCTCCAAGTCAATATAAAATTCTACAGAAAATAGTGTTCTTTTTCTCCAGAAAAT
GCTTGTGAGAATCATTAACCATGTGACAATTTAGAGATTCTTTGTTTTATTTCACTGATTA
ATATACTGTGGCAAATTACACAGATTATTAATTTTTTTTACAAGAGTATAGTATATTTATTT
GAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTGTTATTTCTCAGAATATGGAA
AGAAAATTAATAATGTGTCAATAAATATTTTCTAGAGAGTAA

FIGURE 154

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880

><subunit 1 of 1, 305 aa, 1 stop

><MW: 35383, pI: 5.99, NX(S/T): 0

MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLTAETRVEEAVILTYFPV
VHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQ
WSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREF
PGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWAL
YYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

GAGAGAGGCCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCCTGCCCTGCACTCGGGCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGACCTGTGTGGGGAGGCCCTCCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAGACCGGGAGGATCACAGAGCCAGC**ATG**TTACAGGATCCTGACAGTGATCAACCTCTGAACAGCTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGGATCCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTTGTCTCATCAAGGTGATTCTGGATAAATACTACTTCCCTCTGCGGGCAGCCTCTCCACTTCATCCCGAGGAAGCAGTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTCCCCGAAGGGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGGACTCGGCCACAGGGAACTGGTTCTCTGCCTGTTTTGACAACCTTCACAGAAGCTCTCGCTGAGACAGCCTGTAGGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCAGACCAGGATCTGGA TGTTGTTGAAATCACAGAAAACAGCCAGGAGCTTCGCATGCGGAACTCAAGTGGGCCCTGCTCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCCTGTGGGAAGAGCCTGAAGACCCCCCGTGTGGTGGGTGGGGAGGAGGCCTCTGTGGATTCTTGGCCTTGGCAGGTCAGCATCCAGTACGACAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCTCACGGCAGCCCACTGCTTCAGGAAACATAACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAAACTGGGCAGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCCATGTACCCCAAAGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTCAGGCACAGTCAGGCCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGA TGGGGCTTTACGAAGCAGAATGGAGGGAAGATGTCTGACATACTGCTGCAGGCGTCAGTCCAGGTCATTGACAGCACACGGTGCAATGCAGACGATGCGTACCAGGGGGGAAGTCACCGAGAAGATGATGTGTGCAGGCATCCCGGAAGGGGGTGTGGACACCTGCCAGGGTGACAGTGGTGGGCCCCTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGGCTGCGGGGGCCGAGCACCCAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTG**TAA**TGCTGCTGCCCTTTGCAGTGCTGGGAGCCGCTTCCTTCCTGCCCTGCCACCTGGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCCTTGGGTACACCCCTCTGCCACAGCCTCAGCATTTCTTGGAGCAGCAAAGGGCCTCAATTCCCTGTAAGAGACCTCGCAGCCCAGAGGCGCCAGAGGAAGTCAGCAGCCCTAGCTCGGCCACACTTGGTGCTCCAGCATCCCAGGGAGAGACACAGCCCACTGAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAAGGAACCTTCCCACACTACTGAATGGAAGCAGGCTGTCTTGTAAGGCCAGATCACTGTGGCTGGAGAGGAGAAGGAAAGGTCTGCGCCAGCCCTGTCCGTCTTCACCCATCCCCAAGCCTACTAGAGCAAGAAACCAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTTACCTACTGTTGTCAATTGTTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCTCTGGCAAAAAAAAAAAAAA

FIGURE 156

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885

><subunit 1 of 1, 432 aa, 1 stop

><MW: 47644, pI: 5.18, NX(S/T): 2

MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIIALLSLASIIIVVLIKVILDKYYF
LCGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWF
SACFDNFTEALAETACRQMGYSRAVEIGPDQDLDVVEITENSQELMRNSSGPCLSGSLVSL
HCLACGKSLKTPRVVGEEASVDSWPWQVSIQYDKQHVC GGSILDPHWVLTAAHCFRKHTDV
FNWKVRAGSDKLGSEFSLAVAKIIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFD
EELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPE
GGVDTCQGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL

Transmembrane domain:

amino acids 32-53 (typeII)

158/249

FIGURE 157

GGGCTGAGGCACACTGAGAGACCGGAAAGCCTGGCATTTCCAGAGGGAGGAAACAGCAGCGGCATCCCAGGCTCCAG
AGCTCCCTGGTGACAGTCTGTGGCTGAGC**ATG**GCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCC
TTTTCTCTTCCAACCTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGGAGGCGGGCAGGGGGCCCATGCCCCA
GGGTGAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA
CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGG
ATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTA
AGAAGAAGAGCAATGAGACACAGTGTTCACACTTCATCCGTGTCTGGTTTTCTTACAATGTACCCCATCTCTACA
CCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCTACCTGTTGCCCATCTCGG
AGGACAAGGTGATGGAGGGAAAAGGCCAAAGCCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATG
GGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGC
CTGTCTCAAGACCGACAACCTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCC
AGGTGCTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG
CTAGAGTCTGCAAGAATGACGTGGGCGGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCCAGC
TGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTATCCGCCACGCGGTCTGCTCCCCGCCGATTCCTCCCA
CAGCTCCCCACATCTACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGTTTTGTGCCT
TCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTA
CTTATAGGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCCTCCTCTGATAAGGCCCTGACCT
TCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCCCTGCTGGTGAAATCTGGCGTGGAGTATA
CACGGCTTGCAAGTGGAGACAGCCAGGGCCTTGATGGGCACAGCCATCTTGTATGTACCTGGGAACCACCACAG
GGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGTCTCATCTGGTGGAAGAGATTGAGCTGTTCCCTGACC
CTGAACCTGTTGCAACCTGCAGCTGGCCCCCACCAGGGTGCAGTGTGTTGTAGGCTTCTCAGGAGGTGTCTGGA
GGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTTGGCCGGGACCCCCACTGTGCCT
GGGACCTTGAGTCCCGAACCTGTTGCCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGG
GGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCGCCGAAATCATTA
AAGAAGTCTTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCGCCCCACCTGTCAGCCTTGGCCTCTTATTATT
GGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGG
ATGGAGTTGGGGGTCTCTACCAGTGTCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGG
ACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCATGTGAAGGTCCCGTTGA
CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCTTACTGGCCCCACTTTGTCACTGTCACTGTCCCTCT
TTGCCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGG
TTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGG
AATGCAGGACCTCTGCCAGTGTGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCT**TAA**ACTCTAGGCA
CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGGCCCAAGCACAGCCCTGACTAGGATGACAG
CAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTG
ATGCACAGCAGTCTGCCTCCCCATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTAC
CCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCTC
CAGAAACACAGTGTTCAGAGACCTTAAAAAACCTGCCTGTCCAGGACCCTATGGTAATGAACACCAAAACATC
TAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCAAACTCCCT
TCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTC
TTTCTGAAGTCTGACCACCTTCTTCTTGTCTTCAAGTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG
CAGGGGTAAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCTTTGT
TTTGGGATTGAGAAAACCTGCTTGTGACAGACTGTTTTATTTTTTATTAATAAATAAAGGCTTAAAAAAA

FIGURE 158

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166

><subunit 1 of 1, 761 aa, 1 stop

><MW: 83574, pI: 6.78, NX(S/T): 4

MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKGLQ
DFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKKSNETQC
FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPAHKHTA
VLVDGMLYSGTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPSTQVVYFFFE
ETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLL
PADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPET
NPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVM
YLGTTTGSLSHKAVVSGDSSAHLVEEIQLFDPPEPVRNLQLAPTQGAVFVGFSGGVWRVPRAN
CSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMERGNPEWACASGPMSRSLRP
QSRPQIIKEVLAVPNSILELPCPHLSALASYWWSHGPAAVPEASSTVYNGSLLLIVQDGVGG
LYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWP
HFVTVTVLFLVLVLSGALIILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRT
SASDVDADNNCLGTEVA

Signal peptide:

amino acids 1-30

Transmembrane domains:

amino acids 136-156, 222-247, 474-490, 685-704

FIGURE 159

AGGGTCCCTTAGCCGGGCGCAGGGGCGCGCAGCCAGGCTGAGATCCGCGGCTTCCGTAGAAG
TGAGC**ATG**GCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCTTCTCCCTGGGGTCTGTCTC
TCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGA
CCGGGTTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCACAAAAGAG
GTCTTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCTTGCA
CCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGAAGAACTTTAGG
TGGCAGAGGAAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGCGTTGCAGTGCAGTC
ATTTTTTAAATAGAAAGGATATCATGGATTCTTTAAAGAATGAGAACTTCGACATGGTGATA
GTTGAACTTTTGACTACTGTCTTTCTGATTGCTGAGAAGCTTGGGAAGCCATTTGTGGC
CATTCTTTCCACTTCATTGGGCTCTTTGGAATTTGGGCTACCAATCCCCTTGTCTTATGTTT
CAGTATTCCGTTCTTGTGCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTG
ATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAA
GGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGT
GGTTCATTAACCTCTGACTTTGCCTTTGATTTTGCTCGACCTCTGCTTCCCAACACTGTTTAT
GTTGGAGGCTTGATGGAAAAACCTATTAAACCAGTACCACAAGACTTGGAGAACTTCATTGC
CAAGTTTGGGGACTCTGGTTTTGTCTTGTGACCTTGGGCTCCATGGTGAACACCTGTCAGA
ATCCGGAAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGG
AAGTGTCAGTGTTCTCATTTGGCCCAAAGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGA
CTGGCTTCTCAGAGTGACCTCTGGCTCACCCAAAGCATCCGTCTGTTTGTACCCACGGCG
GGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTT
GGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTAGTT
AAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGAT
ACAAGTCCGCGGCAGTGGCTGCCAGTGTATCTGCGCTCCCACCCGCTCAGCCCCACACAG
CGGCTGGTGGGCTGGATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTA
TGTCTTTTACGACGCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGC
TCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGT
GGGGCCAGAAAGGTGAAGGAGACA**TAA**GGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGG
GCGATGTCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTC
TAGTTATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGC
TAATTTTGTCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT
CTTGTCTCTCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGAATTG
GACCACTGACCCTCAGATTTCCAGCCTTAAAAATCCACCTTCTCTCATGCGCCTCTCCGAA
TCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCCTGCCCC
TACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTTCAAGTTTCTGTTT
TGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTCAAGGC
CGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCACAGTGAGCTCCT
TCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAAAATAAAAGTTTACA
GCGTTATCTCTCCCCAACCTCACTAA

FIGURE 160

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169

><subunit 1 of 1, 523 aa, 1 stop

><MW: 59581, pI: 8.68, NX(S/T): 1

MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRGPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHF
LNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFGSLEFGLPIPLSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCCRQQHMQSTFDNTIKEHFTEGSRPVLSHLLLKAELWF
INSDFAFDFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNP
EIFKEMNNAFAHLPQGVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQ
NSIMEAIQHGVPMVGIPLEFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYK
SAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQYLFDFVFLLGLT
LGTWLWLCGKLLGMAVWWLRGARKVKET

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 483-504

FIGURE 161

GGGCTGTTGATTTGTGGGGGATTTTGAAGAGAGGAGGAATAGGAGGAAGGGGTTGAGGGGCT
 GCCTCTGGCATATGCACACACTCACACATTCTGTACACCCGTCACACACACATACCATGTT
 CTCCATCCCCCAGGTCCAGCCCTCAGTGCTGTCCCATCCAGCAGGGCTACCCTGAAGCTCT
 GGCTGCAGCCCTCCCGTCCAGTGGGCAGGCGGCTTCATCCCTCCTTTCTCTCCCAAAGCCCA
 ACTGCTGTCACTGCATGCTCTGCCAAGGAGGAGGGAAGTGCAGTGACAGCAGGAGTAAGAGT
 GGGAGGCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGGTTTACGCGAGCCTAGAGAGGGC
 AGACTATCAGGGGTGCCGGCGGTGAGAATCCAGGGAGAGGAGCGGAAACAGAAGAGGGGGCAGA
 AGACCGGGGCACTTGTGGGTTGCAGAGCCCCCTCAGCC**ATG**TTGGGAGCCAAGCCACACTGGC
 TACCAGGTCCCCTACACAGTCCCGGGCTGCCCTTGGTTCTGGTGCTTCTGGCCCTGGGGGCC
 GGGTGGGCCCAGGAGGGGTGAGAGCCCGTCCCTGCTGGAGGGGGAGTGCCTGGTGGTCTGTGA
 GCCTGGCCGAGCTGCTGCAGGGGGGGCCCGGGGGAGCAGCCCTGGGAGAGGCACCCCTGGGC
 GAGTGGCATTGCTGCGGTCCGAAGCCACCACCATGAGCCAGCAGGGGAAACCGGCAATGGC
 ACCAGTGGGGCCATCTACTTCGACCAGGTCCCTGGTGAACGAGGGCGGTGGCTTTGACCGGGC
 CTCTGGCTCCTTCGTAGCCCCCTGTCCGGGGTGTCTACAGCTTCCGGTTCCATGTGGTGAAGG
 TGTACAACCGCCAAACTGTCCAGGTGAGCCTGATGCTGAACACGTGGCCTGTCATCTCAGCC
 TTTGCCAATGATCCTGACGTGACCCGGGAGGCAGCCACCAGCTCTGTGCTACTGCCCTTGGA
 CCCTGGGGACCGAGTGTCTCTGCGCCTGCGTCGGGGGAATCTACTGGGTGGTTGGAAATACT
 CAAGTTTCTCTGGCTTCCTCATCTTCCCTCTCT**TGAG**AGGCCCAAGTCTTTCAAGCACAGAAT
 CCAGCCCCGTGACAACCTTCTTCTGCCCTCTCTTGCCCCAGAAACAGCAGAGGCAGGAGAGAG
 ACTCCCTCTGGCTCCTATCCACCTCTTTGCATGGGACCCTGTGCCAAACACCCAAGTTTAA
 GAGAAGAGTAGAGCTGTGGCATCTCCAGACCAGGCCTTTCACCCACCCACCCCAAGTTACC
 CTCCAGCCACCTGCTGCATCTGTTCCCTGCCTGCAGCCCTAGGATCAGGGCAAGGTTTGGCA
 AGAAGGAAGATCTGCACTACTTTGCGGCCTCTGCTCCTCCGGTTCCCCCACCCAGCTTCCT
 GCTCAATGCTGATCAGGGACAGGTGGCGCAGGTGAGCCTGACAGGCCCCCCACAGGAGCCAG
 ATGGACAAGCCTCAGCGTACCCTGCAGGCTTCTTCCCTGTGAGGAAAGCCAGCATCACGGATC
 TCAGCCAGCACCGTCAGAAGCTGAGCCAGCACCGTATGGGCTAGGGTGGGAGGCTCAGCCAC
 AGGCAGAAGGGTGGGAAGGGCCTGGAGTCTGTGGCTGGTGAAGGAAGGAGGGTGTATTG
 TCTAGACTGAACATGGTACACATTCTGCATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCT
 GGCTGTCTTCTATGCTGGATCCCAGATGGACTCTGGCCCTTACCTCCCCACCTGAGATTAG
 GGTGAGTGTGTTTGTCTCTGGCTGAGAGCAGAGCTGAGAGCAGGTATACAGAGCTGGAAGTGG
 ACCATGGAAAACATCGATAACCATGCATCCTCTTGCTTGGCCACCTCCTGAAACTGCTCCAC
 CTTTGAAGTTTGAACCTTTAGTCCCTCCACACTCTGACTGCTGCCTCCTTCCTCCCAGCTCTC
 TCACTGAGTTATCTTCACTGTACCTGTTCCAGCATATCCCCACTATCTCTCTTTCTCCTGAT
 CTGTGCTGTCTTATTCTCCTCCTTAGGCTTCCCTATTACCTGGGATTCCATGATTCACTCCTT
 CAGACCCCTCTCCTGCCAGTATGCTAAACCCCTCCCTCTCTCTTTCTTATCCCGCTGTCCCAT
 GGCCAGCCTGGATGAATCTATCAATAAAACAAGTAGAGAATGGTGGTCAGTGAGACACTAT
 AGAATTACTAAGGAGAAGATGCCTCTGGAGTTTGGATCGGGTGTTACAGGTACAAGTAGGTA
 TGTTGCAGAGGAAAATAAATATCAAACCTGTATACTAAATTAATAA

FIGURE 162

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180

><subunit 1 of 1, 205 aa, 1 stop

><MW: 21521, pI: 7.07, NX(S/T): 1

MLGAKPHWLPGPLHSPGLPLVLVLLALGAGWAQEGSEPVLLERGECLVVCEPGRAAAGGP
GGAALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPV
RGVYSFRFHVVVKVYNRQTVQVSLMLNTWPVISAFANDPDVTREAATSSVLLPLDPGDRV
SLRLRGNLLGGWKYSSFSGFLIFPL

Signal peptide:

amino acids 1-32

164/249

FIGURE 163

[illegible]

FIGURE 164

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184

><subunit 1 of 1, 388 aa, 1 stop

><MW: 43831, pI: 9.64, NX(S/T): 3

MKTLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNRS
KVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLI AVL YFTWL VFDWNTPKKGRRS
QWVRNWAVWRYFRDYFPIQLVKTHNLLTTRNYIFGYHPHGIMGLGAF CNFSTEATEVSKKFP
GIRPYLATLAGNFRMPVLREYLMMSGGICPVSRDTIDYLLSKNGSGNAIIIVVGAAESLSSM
PGKNAVTLRNRKG FVKLALRHGADLVPIYSFGENEVYKQVIFEEGSWGRWVQKKFQKYIGFA
PCIFHGRGLEFSSDTWGLVPYSKPITTVVGEPITIPKLEHPTQQDIDLYHTMYMEALVKLFDK
HKTKFGLPETEVLEVN

Important features of the protein:**Transmembrane domain:**

amino acids 76-97

N-glycosylation sites.

amino acids 60-63, 173-176, 228-231

N-myristoylation sites.

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-
245, 318-323, 378-383

FIGURE 165

GGGCGCGGGGATGGGGGCGGGGGCGGGCGGGCGCGCACTCGCTGAGGCCCGACGACGAGGCCGGGGCGGGGCCA
GGGCCGAGGAGCGCGGCGGCCAGAGCGGGGCGCGGAGGCGACGCCGGGGACGCCCGCGCGACGAGCAGGTGGCG
GCGGCTGCAGGCTTGTCCAGCCGGAAGCCCTGAGGGCAGCTGTTCCCACTGGCTCTGCTGACCTTGTGCCTTGG
CGGCTGTCTCAGCGAGGGGGCCGTGCACCCGCTCCTGAGCAGCGCCATGGCCCTGCTGGCCTTCTCTGAAGACCCA
GTTCTGTCTGCACCTGCTGGTCTGGCTTTGTCTTCGTGGTGAGTGGTCTGGTCATCAACTTCGTCCAGCTGTGCAC
GCTGGCGCTCTGGCCGGTCAGCAAGCAGCTCTACCGCCGCCCTCAACTGCCGCCTCGCCTACTCACTCTGGAGCCA
ACTGGTCATGCTGCTGGAGTGGTGGTCTCTGCACGGAGTGACACTGTTACACGGACCAGGCCACGGTAGAGCGCTT
TGGGAAGGAGCACGCAGTCATCATCCTCAACCACAACCTTCGAGATCGACTTCCTCTGTGGGTGGACCATGTGTGA
GCGCTTCGGAGTGCTGGGGAGCTCCAAGGTCTCGCTAAGAAGGAGCTGCTCTACGTGCCCCCTCATCGGCTGGAC
GTGGTACTTTCTGGAGATTGTGTTCTGCAAGCGGAAGTGGGAGGAGGACCGGGACACCGTGGTCGAAGGGCTGAG
GCGCCTGTCTGGACTACCCCGAGTACATGTGGTTTTCTCCTGTACTGCGAGGGGACGCGCTTCACGGAGACCAAGCA
CCGCGTTAGCATGGAGGTGGCGGCTGCTAAGGGGCTTCCTGTCTCAAGTACCACCTGCTGCCGCGGACCAAGGG
CTTCACCACCGCAGTCAAGTGCCCTCCGGGGGACAGTCGCAGCTGTCTATGATGTAACCCCTGAACCTCAGAGGAAA
CAAGAACCCGTCCTGCTGGGGATCCTCTACGGGAAGAAGTACGAGGCGGACATGTGCGTGAGGAGATTTCTCT
GGAAGACATCCCGCTGGATGAAAAGGAAGCAGCTCAGTGGCTTCATAAACTGTACCAGGAGAAGGACGCGCTCCA
GGAGATATATAATCAGAAGGGCATGTTTCCAGGGGAGCAGTTTAAGCCTGCCCGGAGGCCGTGGACCCTCCTGAA
CTTCCTGTCTGGGCCACCATTCTCCTGTCTCCCTCTTCAGTTTTGTCTTGGGCGTCTTGGCAGCGGATCACC
TCTCCTGATCCTGACTTTCTTGGGGTTTGTGGGAGCAGCTTCCTTTGGAGTTCGCAGACTGATAGGAGAATCGCT
TGAACCTGGGAGGTGGAGATTGCAGTGAAGCTGAGATGGCATCACTGTACTCCAGCCTAGGCAACAGAGCAAGACT
CAGTCTCAAAAAAAAAAAAAAAAAACAAAAAACCCAGAAATTCCTGGAGTTGAACTGTGTAGTTACTGACATGAAAA
ATTCACTAGAGGCTGAACAGCAGATTTGAGCAGGCAGAAAAAATCAGCAAGCTTGAAGATGGTACCTTGAGATT
TTTCAGGCTAATGAAAAAGAATGAAGGAAAATTAACAGCCTCAGAGACCCATGGTGCACCGTCACACAAATCAA
CATATGCATGATGAGAGTCCCAGAAGGAGAGGAGAGAAAGGGTCAGAAAGAATGGCCACAAGCTGATGAAAAACA
GTAACCTACCCACTCAGGAAGCTCAGTGAACCTCAATGAGGATGAATATCAGAGATCCACACCTAGATATTTTCA
AATCAAAGTGTCAAATGACAAAGAATCTTGAAAGCAGCAAGAGATGAGCAACTTATCTTGTTCAAAGGATCTTTG
ATCAGATTAACAGCTCATTTCTCCTCAGAAATCATGGGAGCCAGGAGATAGTGGGATGAACACTGTTGAAGGCAA
AACCTTCAACTGTAATTATTGGACTTTTGGAGTCTTAGATGGTCTGACCTCTTTGTCTTCAGGGACAGTTTTTCA
ATTTAATCCCTAATAACAATTAGTCAAGCTTCCTTGACCTGTAGGAAGGCCTGTCTTTAGGCCGGGCACAGTGGC
TTACACCTGTAATCCCAGCACTTTGGGAGGCCCAGACGGGTGGATCATTTGGGGTCAGGCTGATCTCAAACCTCCT
GAGTTCAAGTGATCTGCCCGCCTCAGCCTCCCAAAGTGTTGTGATTGCAGGCGTGAGCCACTGCGCCTGGCCGGA
ATTTCTTTTTTAAGGCTGAATGATGGGGGCCAGGCACGATGGCTCACGCCTGTGATCCCAAGTAGCTTGGATTGTA
AACATGCACCACCATGCCTGGCTAATTTTTGTATTTTTTAGTAGAGACGTGTTAGCCAGGCTGGTCTCGATCTCCT
GACCTCAAGTGACCACCTGCCCTCAGCCTCCCAAAGTACTGGGATTACAGGCGTGAGCCACTGTGCCTGGCCTTGA
GCATCTTGTGATGTGCTTATTGGCCATTTGTATATCTTCTATCTTCTTTGGGGAATGTCTGTTCAAGTCTTTG
CCTTTTTTAAATTTTTATTTATTTATTTATTTATTTATTTTGGAGACAGGGTCTTGTCTGTTGCCAGGCTGGAGTA
CAGTGGCACAGTCTTGGCTCACTGCAGCCTCGACCTCCTGGGCTGCAGTGATCCTCCACCTCAGCCTCCCTTGT
AGCTGTATTTTTTTGTATTTTGTATTTTGTAGCTGTAGTTTTTGTATTTTTTGTGGAGACAGCATTTACCATGA
TGCCCAGGCTGGTCTTGAACCTCCTGAGCTCAAGTGATCTGCCTGCTTCAGCCTCCCAAAGTGCTGGGATTACAGA
CATGAGCCACTGCACCTGGCAAACCTCCCAAATTAACACACACACACAAAAAACCACTGATTCAAATGGGCA
GAGGGGCCGGGTGTGGCCCCAACTACCAGGGAGACTGAAGTGGGAGGATCGCTTGGGCATGAGAAGTCGAGGCTG
CAGTGAGTCGAGGTTGTGCGACTGCATTCCAGCCTGGACAACAGAGTGAGACCCTGTCTC

FIGURE 166

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213

><subunit 1 of 1, 368 aa, 1 stop

><MW: 42550, pI: 9.11, NX(S/T): 1

MGLLAFLKTQFVLHLLVGFFVVSGLVINQVQLCTLALWPVSKQLYRRLNCRSLAYSLWSQLV
MLLEWWSCTECTLFQATVERFGKEHAVIILNHNFEIDFLCGWTMCERFGVLGSSKVLAKK
ELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHR
VSMEVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAAVYDVTLLNFRGNKNPSLLGILYGKK
YEADMVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLN
FLSWATILLSPLFSFVLGVFASGSPLLILTFLGFVGAASFGVRRRLIGESLEPGRWRLQ

Important features of the protein:**Signal peptide:**

amino acids 1-25

Transmembrane domains:

amino acids 307-323, 335-352

Tyrosine kinase phosphorylation sites.

amino acids 160-168, 161-169

FIGURE 167

GATATTCTTTATTTTAAAGAATCTGAAGTACTATGCATCACTCCCTCCAATGTCCTGGGGCA
GCCACCAGGCATATTCATCTTTGTGTGTGTTTTCTTTGCTTTAGCACTGGGGCACTTCTT
GCTTATTTCTTTGGTAGGAAAGGGGCTCAGTTTGTCTTGTGGGGTTGGTGGCAGGCAGGCCG
GCTTACGCCTGATACGGCCCTGGGTTAGAAGGGAAGGGAAGATAAACTTTTATACAAATGGG
GATAGCTGGGGTCTGAGACCTGCTTCCTCAGTAAATTCCTGGGATCTGCCTATACCTTCTT
TTCTCTAACCTGGCATAACCTGCTTAAAGCCTCTCAGGGCTTCTCTCTGTTCTTAGGATCAA
AGTATTTAGAGCTACAAGAGCCCTCATGGTCTGGCCCCTGCCCCCTGGCCAGCTTCATTGT
ACATGTGGTGTCTCTTGTCTGTTCTCTGTAATGTGGTATGCCATGGGGTCTTTGCACAAGCCT
TTCCTCTTTGGCTGGACACTGTTCCCTGCCCCCCCCATACTCTTCCTACTTAATATGTAGTC
ATCCTGCAGATTTCAATTCTAACATCATTTTCTCCAGGGATCCTGGCCTGACAGAATCTCAT
CTTGTTTAATGCTCTCATAAGACCACTTGTTTCCCTTTTGCAGCACTTGCCACTCAGTTGTA
TCTTTATGTGCGTTTGTGGTTGTATGGGTTGTGTCTGTTCCCCAGAATGCCAGCTCTGAGC
TGCGTGAGGGTCAAGGGCATTGCTGTGCCTGCCAGGTATAGTGCCTACATGTGGTGGGTGCT
CATGTTTTAGAGACTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTTCACCA
GATGGTGTAGGGCCCAGCATTGTAAATTACACGTTGACTGTGCTTGTGAATTATCTGGGGA
TGCAGGTCCTGATTCAGTAGGCCAGGTTGGGCATCTCTAACAACTCCCACGTGATGCTGA
TGCTGGTCCTATGAACTATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGGTGGC
TCACACCTATGATCCCAGCACTTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATT
TCAAGACTAGCCTGGCCAACATGGTGGAAACCCCATCTGTACTAAAAATACACAAATTAGCTG
GGCATGGTGGCACATGCCTGTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTG
AACCTGGGAGGCGGAGGTTGCAGTGAGCCGAGATCAGGCCACTGTATTCCAACCAGGGTGAC
AGAGTGAGACTCTATGTCCAAAAAAAAAAAAA

FIGURE 168

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234

><subunit 1 of 1, 143 aa, 1 stop

><MW: 15624, pI: 9.58, NX(S/T): 0

MHHSLQCPGAATRHIHLCVCFSFALALGHFLLISLVGKGLSLSCGVGGRQAGLRRLIRPWVRR
EGKINFYTNGDSWGLRPASSVKFLGSAYTFFSLTWHTLLKASQGFSLFLGSKYLELQEPSWS
GPCPPGQLHCTCGVLLSFL

Important features of the protein:

Signal peptide:

amino acids 1-28

170/249

FIGURE 169

GGCTGGACTGGAACCTCCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGA
TTATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACTTTTTTCAGCAACTAAAAAGCCAC
AGGAGTTGAACTGCTAGGATTCTGACT**ATG**CTGTGGTGGCTAGTGCTCCTACTCCTACCTAC
ATTAAAATCTGTTTTTTGTTCTCTTGTAAC TAGCCTTTACCTTCCTAACACAGAGGATCTGT
CACTGTGGCTCTGGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCAC
ACCGTCCCCCTCGAAGCCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTC
ACCAACTGTCTCACGTCTGGAGGCACTGACTCGGGCAGTGCAGGTAGCTGAGCCTCTTGTA
GCTGCGGCTTTCAAGGTGGGCCTTGCCCTGGCCGTAGAAGGGAT**TGA**CAAGCCCGAAGATTT
CATAGGCGATGGCTCCCACTGCCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGG
CCAGGACGGGCGGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCCCGCCAT
CTAACCTTTTCATGTCTGCACATCACCTGATCCATGGGCTAATCTGAACTCTGTCCCAAGG
AACCAGAGCTTGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTT
TATGTGACAGGACTTGCAATTCTCCTGGAACATGAGGGAACGCCGAGGAAAGCAAAGTGGCA
GGGAAGGAACCTTGTGCCAAATTATGGGTCAGAAAAGATGGAGGTGTTGGGTTATCACAAGGC
ATCGAGTCTCCTGCATTCACTGAGGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACT
CGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCCGATCCACGTACCAGCTGCTG
AAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCGATCACCAG
CCAGGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCCCTCCTTCCCTC
TGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGCTAATG
GCTCAGTGTTGGCCCAGGAGGTGAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCTGTGCG
AACACGGAAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGGCT
CAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGT
TCAAATGATCTCCAAGGGCCCTTATACCCCAGGAGACTTTGATTTGAATTTGAAACCCCAA
TCCAAACCTAAGAACCAGGTGCATTAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATG
CCAACATTTTGGGAGGCCGAGGCGGGTAGATCACCTGAGGTCAGGAGTTCAAGACCAGCCTG
GCCAACATGGTGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGT
GTGTGCCTGTATCCCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGT
GAAGGAGGCTGAGACAGGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGA
AAAAATAAAAAAAGAATTATGGTTATTTGTAA

FIGURE 170

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277
><subunit 1 of 1, 109 aa, 1 stop
><MW: 11822, pI: 8.63, NX(S/T): 0
MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTA
SPCWPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRD
```

Signal peptide:

amino acids 1-15

172/249

FIGURE 171

GCGGGCCCGCGAGTCCGAGACCTGTCCCAGGAGCTCCAGCTCACGTGACCTGTCACTGCCTC
 CCGCCGCCTCCTGCCCGCGCC**ATG**ACCCAGCCGGTGCCCCGGCTCTCCGTGCCCGCCGCGCT
 GGCCCTGGGCTCAGCCGCACTGGGCGCCGCCTTCGCCACTGGCCTCTTCCTGGGGAGGCGGT
 GCCCCCATGGCGAGGCCGGCGAGAGCAGTGCCTGCTTCCCCCGAGGACAGCCGCCTGTGG
 CAGTATCTTCTGAGCCGCTCCATGCGGGAGCACCCGGCGCTGCGAAGCCTGAGGCTGCTGAC
 CCTGGAGCAGCCGCAGGGGGATTCTATGATGACCTGCGAGCAGGCCAGCTCTTGGCCAACC
 TGGCGCGGCTCATCCAGGCCAAGAAGGCGCTGGACCTGGGACCTTCACGGGCTACTCCGCC
 CTGGCCCTGGCCCTGGCGCTGCCCGCGGACGGGCGCGTGTTGACCTGCGAGGTGGACGCGCA
 GCCCCCGGAGCTGGGACGGCCCCCTGTGGAGGCAGGCCGAGGCGGAGCACAAAGATCGACCTCC
 GGCTGAAGCCCGCCTTGGAGACCCTGGACGAGCTGCTGGCGGCGGGCGAGGCCGGCACCTTC
 GACGTGGCCGTGGTGGATGCGGACAAGGAGAACTGCTCCGCCTACTACGAGCGCTGCCTGCA
 GCTGCTGCGACCCGGAGGCATCCTCGCCGTCCTCAGAGTCCTGTGGCGCGGGAAGGTGCTGC
 AACCTCCGAAAGGGGACGTGGCGGCCGAGTGTGTGCGAAACCTAAACGAACGCATCCGGCGG
 GACGTCAGGGTCTACATCAGCCTCCTGCCCCCTGGGCGATGGACTCACCTTGGCCTTCAAGAT
CTAGGGCTGGCCCCCTAGTGAGTGGGCTCGAGGGAGGGTTGCCTGGGAACCCCAGGAATTGAC
 CCTGAGTTTTTAAATTCGAAAATAAAGTGGGGCTGGGACACAAAAAAAAAAAAAAAAAAAA

173/249
 GCGGGCCCGCGAGTCCGAGACCTGTCCCAGGAGCTCCAGCTCACGTGACCTGTCACTGCCTC
 CCGCCGCCTCCTGCCCGCGCC**ATG**ACCCAGCCGGTGCCCCGGCTCTCCGTGCCCGCCGCGCT
 GGCCCTGGGCTCAGCCGCACTGGGCGCCGCCTTCGCCACTGGCCTCTTCCTGGGGAGGCGGT
 GCCCCCATGGCGAGGCCGGCGAGAGCAGTGCCTGCTTCCCCCGAGGACAGCCGCCTGTGG
 CAGTATCTTCTGAGCCGCTCCATGCGGGAGCACCCGGCGCTGCGAAGCCTGAGGCTGCTGAC
 CCTGGAGCAGCCGCAGGGGGATTCTATGATGACCTGCGAGCAGGCCAGCTCTTGGCCAACC
 TGGCGCGGCTCATCCAGGCCAAGAAGGCGCTGGACCTGGGACCTTCACGGGCTACTCCGCC
 CTGGCCCTGGCCCTGGCGCTGCCCGCGGACGGGCGCGTGTTGACCTGCGAGGTGGACGCGCA
 GCCCCCGGAGCTGGGACGGCCCCCTGTGGAGGCAGGCCGAGGCGGAGCACAAAGATCGACCTCC
 GGCTGAAGCCCGCCTTGGAGACCCTGGACGAGCTGCTGGCGGCGGGCGAGGCCGGCACCTTC
 GACGTGGCCGTGGTGGATGCGGACAAGGAGAACTGCTCCGCCTACTACGAGCGCTGCCTGCA
 GCTGCTGCGACCCGGAGGCATCCTCGCCGTCCTCAGAGTCCTGTGGCGCGGGAAGGTGCTGC
 AACCTCCGAAAGGGGACGTGGCGGCCGAGTGTGTGCGAAACCTAAACGAACGCATCCGGCGG
 GACGTCAGGGTCTACATCAGCCTCCTGCCCCCTGGGCGATGGACTCACCTTGGCCTTCAAGAT
CTAGGGCTGGCCCCCTAGTGAGTGGGCTCGAGGGAGGGTTGCCTGGGAACCCCAGGAATTGAC
 CCTGAGTTTTTAAATTCGAAAATAAAGTGGGGCTGGGACACAAAAAAAAAAAAAAAAAAAA

FIGURE 172

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282

><subunit 1 of 1, 262 aa, 1 stop

><MW: 28809, pI: 8.80, NX(S/T): 1

MTQPVPRLSVPAALALGSAALGAAFATGLFLGRRCPPWRGRREQCLLPEDSRLWQYLLSRS
MREHPALRSLRLLTLEQPQGDMMTCEQAQLLANLARLIQAKKALDLGTFTGYALALALAL
PADGRVVTCEVDAQPPELGRPLWRQAEAEHKIDRLKPALETLDELLAAGEAGTFDVAVVDA
DKENC SAYYERCLQLLRPGGILAVLRVLWRGKVLQPPKGDVAAECVRNLNERIRRDVRVYIS
LLPLGDGLTLAFKI

Important features of the protein:**Signal peptide:**

amino acids 1-25

Transmembrane domains:

amino acids 8-30, 109-130

N-glycosylation site.

amino acids 190-193

Tyrosine kinase phosphorylation site.

amino acids 238-246

N-myristoylation sites.

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

Amidation sites.

amino acids 31-34, 39-42

FIGURE 173

CCGCCGCCGACGCCGCTACCGCCGCTGCAGCCGCTTTCCGCGGCCTGGGCCTCTCGCCGTCA
 GC**ATG**CCACACGCCTTCAAGCCCCGGGGACTTGGTGTTTCGCTAAGATGAAGGGCTACCCTCAC
 TGGCCTGCCAGGATCGACGACATCGCGGATGGCGCCGTGAAGCCCCACCCAACAAGTACCC
 CATCTTTTCTTTGGCACACACGAAACAGCCTTCCTGGGACCCAAGGACCTGTTCCCTACG
 ACAAATGTAAAGACAAGTACGGGAAGCCCAACAAGAGGAAAGGCTTCAATGAAGGGCTGTGG
 GAGATCCAGAACAACCCCCACGCCAGCTACAGCGCCCCCTCCGCCAGTGAGCTCCTCCGACAG
 CGAGGCCCCCGAGGCCAACCCCGCCGACGGCAGTGACGCTGACGAGGACGATGAGGACCGGG
 GGGTCATGGCCGTACAGCGGTAACCGCCACAGCTGCCAGCGACAGGATGGAGAGCGACTCA
 GACTCAGACAAGAGTAGCGACAACAGTGGCCTGAAGAGGAAGACGCCTGCGCTAAAGATGTC
 GGTCTCGAAACGAGCCCCGAAAGGCCTCCAGCGACCTGGATCAGGCCAGCGTGTCCCATCCG
 AAGAGGAGAACTCGGAAAGCTCATCTGAGTCGGAGAAGACCAGCGACCAGGACTTCACACCT
 GAGAAGAAAGCAGCGGTCCGGGCGCCACGGAGGGGGCCCTCTGGGGGGACGGAAAAAAGAA
 GGCGCCGTACGCTCCGACTCCGACTCCAAGGCCGATTCCGACGGGGCCAAGCCTGAGCCGG
 TGGCCATGGCGCGGTTCGGCGTCTCCTCCTCCTCTTCTCCTCCTCCTCCGACTCCGATGTG
 TCTGTGAAGAAGCCTCCGAGGGGGCAGGAAGCCAGCGGAGAAGCCTCTCCCGAAGCCGCGAGG
 GCGGAAACCGAAGCCTGAACGGCCTCCGTCCAGCTCCAGCAGTGACAGTGACAGCGACGAGG
 TGGACCGCATCAGTGAGTGGAAGCGGCGGGACGAGGCGCGGAGGCGCGAGCTGGAGGCCCCG
 CGGCGGCGAGAGCAGGAGGAGGAGCTGCGGCGCCTGCGGGAGCAGGAGAAGGAGGAGAAGGA
 GCGGAGGCGCGAGCGGGCCGACCGCGGGGAGGCTGAGCGGGGCAGCGGCGGCAGCAGCGGGG
 ACGAGCTCAGGGAGGACGATGAGCCCGTCAAGAAGCGGGGACGCAAGGGCCGGGGCCGGGGT
 CCCCCGTCTCCTCTGACTCCGAGCCCGAGGCCGAGCTGGAGAGAGAGGCCAAGAAATCAGC
 GAAGAAGCCGCAGTCTCAAGCACAGAGCCCCGCCAGGAAACCTGGCCAGAAGGAGAAGAGAG
 TGCGGCCCCGAGGAGAAGCAACAAGCCAAGCCCGTGAAGGTGGAGCGGACCCGGAAGCGGTCC
 GAGGGCTTCTCGATGGACAGGAAGGTAGAGAAGAAGAAAGAGCCCTCCGTGGAGGAGAAGCT
 GCAGAAGCTGCACAGTGAGATCAAGTTTGCCCTAAAGGTCGACAGCCCCGACGTGAAGAGGT
 GCCTGAATGCCCTAGAGGAGCTGGGAACCCTGCAGGTGACCTCTCAGATCCTCCAGAAGAAC
 ACAGACGTGGTGGCCACCTTGAAGAAGATTGCGCGGTACAAAGCGAACAAGGACGTAATGGA
 GAAGGCAGCAGAAGTCTATACCCGGCTCAAGTCGCGGGTCTCGGCCCAAAGATCGAGGCGG
 TGCAGAAAGTGAACAAGGCTGGGATGGAGAAGGAGAAGGCCGAGGAGAAGCTGGCCGGGGAG
 GAGCTGGCCGGGGAGGAGGCCCCCCCAGGAGAAGGCGGAGGACAAGCCCAGCACCGATCTCTC
 AGCCCCAGTGAATGGCGAGGCCACATCACAGAAGGGGGAGAGCGCAGAGGACAAGGAGCACG
 AGGAGGGTCGGGACTCGGAGGAGGGGCCAAGGTGTGGCTCCTCTGAAGACCTGCACGACAGC
 GTACGGGAGGGTCCCGACCTGGACAGGCCTGGGAGCGACCGGCAGGAGCGCGAGAGGGCACG
 GGGGACTCGGAGGCCCTGGACGAGGAGAGCT**TGA**GCCGCGGGCAGCCAGGCCCAGCCCCCGC
 CCGAGCTCAGGCTGCCCCCTCCTTCCCCGGCTCGCAGGAGAGCAGAGCAGAGAACTGTGGG
 GAACGCTGTGCTGTTTGTATTTGTTCCCTTGGGTTTTTTTTTCTGCCTAATTTCTGTGATT
 TCCAACCAACATGAAATGACTATAAACGGTTTTTTAATGA

FIGURE 174

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286

><subunit 1 of 1, 671 aa, 1 stop

><MW: 74317, pI: 7.61, NX(S/T): 0

MPHAFKPGDLVFAKMGYPHWPARIDDIADGAVKPPPNKYPIFFFGTHETAFLGPKDLFPYD
KCKDKYGKPNKRKGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDDEDRG
VMAVTAVTATAASDRMESDSDSDKSSDNSGLKRKTPALKMSVSKRARKASSDLQASVSPSE
EENSESSSESEKTSQDFTPEKKA AVRAPRRGPLGGRKKKKAPSASDSDSKADSDGAKPEPV
AMARSASSSSSSSSSSSDSDSVVKKPPRGRKPAEKPLPKPRGRKPKPERPPSSSSSSSDSDSDEV
DRISEWKRRDEARRRELEARRRREQEEELRRLREQEKEEKERRRERADRGEAERGSGGSSGD
ELREDDEPVKKRGRKGRGRGPPSSSDSEPEAELEREAKKS AKKPQSSSTEPARKPGQKEKRV
RPEEKQQA KPVKVERTRKRSEGF SMDRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRC
LNALEELGTLQVTSQILQKNTDVVATLKKIRRYKANKDVM EKAAEVYTRLKSRVLGPKIEAV
QKVNKAGMEKEKAEK LAGEELAGEEAPQEKAEDKPSTDLSAPVNGEATSQKGESAEDKEHE
EGRDSEEGPRCGSSEDLHDSVREGPD LDRPGSDRQERERARGDSEALDEES

Signal peptide:

amino acids 1-13

GTITGGTTCTCCTGGATCTTACCTTACCAACTGCAGATCTTGGGACTCATCAGCCTCAATAATTATATTAATTAATTAACACCATTTGAAAGAGAACATTGTTTTTTCATCATGAATGCTAATAAAGATGAAAGACTTAAAGCCAGAAAGCCAAGA
TTTTTACCTTTTTTCTGCTTTGATGATGCTAAGCATGACCATGTTGTTTTCTTCCAGTCACTGGCACTTTGAAGCA
AAATATTTCCAAGACTCAAGCTAACCTACAAAGACTTGTGCTTTCAAATAGCTGTATTTCCCTTTTTGGGTTTCATC
AGAAGGACTGGATTTTCAAACCTCTTCTCTTAGATGAGGAAAGAGGCCAGGCTGCTCTTGGGAGCCAAAGACCACAT
CTTTCTACTCAGTCTGGTTGACTTTAAACAAAAATTTTAAAGAAATTTATTTGGCCTGCTGCAAAAGGAACGGGTGGA
TTTATGTAATTTAGCTGGGAAAGATGCCAATACAGAATGTGCAAAATTTTCATCAGAGTACTTCAGCCCTATAACAA
AACTCACATATATGTGTGTGGAACCTGGAGCATTTCATCCAATATGTGGGTATATTGATCTTGGAGTCTACAAGGA
GGATATTATATTCAAACCTAGACACACATAATTTGGAGTCTGGCAGACTGAAATGTCTTTTCGATCCTCAGCAGCC
TTTTGCTTCAGTAATGACAGATGAGTACCTCTACTCTGGAACAGCTTCTGATTTCTTGGCAAAGATACTGCAI
CACTCGATCCCTTGGGCCCTACTCATGACCACCACATACATCAGAACTGACATTTTCAGAGCACTACTGGCTCAATGG
AGCAAAATTTTATTTGGAACCTTTCTTCTATACCAGACACCTACAAATCCAGATGATGATAAAATATATTTCTTCTTTG
TGAATCATCTCAAGAAGGCAGTACCTCCGATAAAACCATCCTTTCTCGAGTTGGAAGAGTTTGTAAAGAAATGATGT
AGGAGGACAACGCAGCCTGATAAAACAAGTGGACGACTTTTCTTAAAGGCCAGACTGATTTGCTCAATTCCTGGAAG
TGATGGGGCAGATACTTACTTTTGATGAGCTTCAAGATATTTATTTACTCCCCACAAGAGATGAAAGAAATCCTGT
AGTATATGGAGTCTTTACTACAACAGCAGCTCCATCTTCAAAGGCTCTGCTGTTGTGTGTATAGCATGGCTGACAT
CAGAGCAGTTTTTAAATGGTCCATATGCTCATAAGGAAAGTGACAGCATTGTTGGGTGAGTATGATGGGGAAT
TCCTTATCCACGGCCTGGTACATGCTCAAAGCAAAACCTATGACCCACTGAITTAAGTCCACCCGAGATTTTCCAGA
TGATGTCATCAGTTTCATAAAGCGGCACCTCTGTGATGTATAAGTCCGTATACCCAGTTGCAGGAGGACCAACGTT
CAAGAGAATCAATGTGGATTACAGACTGACACAGATAGTGGTGGATCATGTTCATTGCAGAAGATGGCCAGTACGA
TGTAATGTTTTCTTGGAAACAGACATTTGGAACCTGTCTCAAAGTTGTGAGCATTTCAAAGGAAAAGTGGAAATATGGA
AGAGGTAGTGTCTGGAGGAGTTGCAGATATTTCAAGCACTCATCAATCATCTTGAACATGGAATTTGTCTGAAGCA
GCAACAATTTGATCAATTTGGTTCCCGAGATGGATTGTTTTCAGCTCTCTTGCACAGATGCGCACTTTATGGGAAAGC
TTCGCGCAGACTGTTGTCTTCCAGAGACCCCTACTGTGCTGGGATGGAAATGCATGCTCTCGATATGCTCCTAC
TTCTAAAAGGAGAGCTAGACGCCAAGATGTAAATATGGCGACCCCAATCACCAGTGTCTGGGACATCGAAGACAG
CATTAGTCATGAACTGCTGATGAAAAGGTGATTTTTGGCATTGAATTTAACTCAACCTTTCTGGAATGTATACC
TAAATCCCAACAGCAACTATTTAAATGGTATATCCAGAGGCTCAGGGGATGAGCATCGAGAGGAGTTGAAGCCCGA
TGAAGAATCATCAAAACGGAATATGGGCTACTGATTCGAAGTTTGCAGAAGAAGGATCTGGGATGTATTACTG
CAAGGCCAGGAGCACACTTTTCATCCACACCATAGTGAAGCTGACTTTGAATGTCAATTGAGAATGAACAGATGGA
AAATACCCAGAGGGCAGAGCATGAGGAGGGGCAGGTCAAGGATCTATTGGCTGAGTCACGGTTGAGATACAAAGA
CTACATCCAAATCCTTAGCAGCCCAAACCTTCAGCCTCGACCAGTACTGCGAACAGATGTGGCACAGGGAGAAGCG
GAGACAGAGAAACAAGGGGGGGCCCAAAGTGGAAGCACATGCAGGAATGAAGAAGAAACGAAATCGAAGACATCA
CAGAGACCTGGATGAGCTCCCTAGAGCTGTAGCCACGTTAGTTTTCTACTTAATTTAAAGAAAAGAAATCCTTACC
TATAAAACATATGCTTCTGTTTTGTATATCCCTTATAGTAATTCATAAATGCTTCCCATGGAGTTTGTCTAAGG
CACAAGACAATAATCTGAATAAGACAATATGTGATGAATATAAGAAGGGCAAAAAATTCATTTGAACCAAGTTTTT
CCAAGAACAATCTTGCACAAGCAAAGTATAAGAATTATCCTAAAAATAGGGGGTTTTACAGTTGTAAATGTTTTA
TGTTTTGAGTTTTTGAATTTTATTGTTCATGTAAATAGTTGAGCTAAGCAAGCCCCGAATTTGATAGTGTATAAGGT
GCTTTATTTCCCTCGAATGTCCATTAAGCATGGAATTTACCATGCAAGTTGTGCTATGTTCTTATGAACAGATATAT
CATTCCTATTGAGAACCAGCTACCTTTGTGGTAGGGAATAAGAGTGCAGACAAATTAAGACAACCTCCCATTATC
AACAGGAACCTTTCTCAGTGAGCCATTCTCTCTGGAGAATGGTATAGGAATTTGGAGAGGTGCATTATTTCTTTC
TGGCCACTGGGGTTAAATTTAGTGTACTACAACATTGATTTACTGAAGGGCACTAATGTTTTCCCCCAGGATTTCT
ATTGACTAGTCAGGAGTAACAGGTTTCACAGAGAGAAGTTGGTGCTTAGTTATGTGTTTTTTAGAGTATATACTAA
GCTCTACAGGGACAGAATGCTTAAATAAATACTTTAATAAGATATGGGAAAATATTTTAAATAAAACAAGGAAAACA
TAATGATGTATAATGCATCTGTATGGGAAGGCATGCAGATGGGATTTGTTAGAAGACAGAAGGAAAGACAGCCAT
AAATTTCTGGCTTTGGGGAAAACATCATATCCCCATGAAAGGAAGAACAATCACAATAAAGTGAGAGTAATGTAA
TGGAGCTCTTTTCTACTAGGGGTAAAGTAGCTGCCAATTTGTAATTCATCTGTTAAAAAAAATCTAGATTATAACA
AACTGCTAGCAAAATCTGAGGAAACATAAATTTCTTCTGAAGAATCATAGGAAGAGTAGACATTTTTATTTATAACC
AATGATATTTTCAGTATATATTTTTCTCTCTTTTAAAAAATATTTATCATACTCTGTATATTATTTCTTTTTACTGC
CTTTATTTCTCTCCTGTATATTGGATTTTGTGATTATATTTGAGTGAATAGGAGAAAACAATATATAACACACAGA
GAATTAAGAAAATGACATTTCTGGGGAGTGGGGATATATTTGTTGAATAACAGAACGAGTGTAAAATTTTAAAC
AACGGAAGGGTTAAATTAACCTTTTGACATCTTACTCAACCTTTCTCATTGCTGAGTTAATCTGTTGTAATT
GTAGTATTGTTTTTGAATTTTAAACAATAAATAAGCCTGCTACATGT

FIGURE 176

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883

><subunit 1 of 1, 777 aa, 1 stop

><MW: 89651, pI: 7.97, NX(S/T): 3

MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNIPLRLKLTyKDLLLSNSCIPFL
 GSSEGLDFQTLILLDEERGRLLLGAKDHI FLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDA
 NTECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRLKCPFD
 PQQPFASVMTDEYLYSGTASDFLGKDTAFTRSLGPTHDDHYIRTDISEHYWLN GAKFIGTFF
 IPDTYNPDDDKIYFFFRESSQEGSTSDKTILSRVGRVCKNDVGGQ RSLINKWTTFLKARLIC
 SIPGSDGADTYFDELQDIYLLPTRDERNPVVYGVFTTTSSIFKGSAVCVYSMADIRAVFNGP
 YAHKESADHRWVQYDGRIPYPRPGTCPSKTYDPLIKSTRDFPDDVISFIKRHSVMYKSVYPV
 AGGPTFKRINVDYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVVSISKEKWNMEEVVLEE
 LQIFKHSSIIILNMELSLKQQQLYIGSRDGLVQLSLHRCDTY GKACADCCLARDPYCAWDGNA
 CSRYAPTSKRRARRQDVKYGDPITQCWDIEDSISHETADEKVIFGIEFNSTFLECIPKSQQA
 TIKWYIQRSGDEHREELKPDERIIKTEYGLLIRSLQKKDSGMY YCKAQEHTFIHTIVKLTLN
 VIENEQMENTQRAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRN
 KGGPKWKHMQEMKKKRNRHRDLDELPRAVAT

Important features of the protein:

Signal peptide:

amino acids 1-36

N-glycosylation sites.

amino acids 139-142, 607-610, 724-727

Tyrosine kinase phosphorylation site.

amino acids 571-576

Gram-positive cocci surface proteins 'anchoring' hexapeptide.

amino acids 32-37

FIGURE 177

CCCTGACCTCCCTGAGCCACACTGAGCTGGAAGCCGCAGAGGTATCCTGGAGCATGCCACCGCGGGGAGCAGA
CAACCTCCCAGGTAAGCTGGGAGCAAGACCTGAAGCTGTTTCTTCAGGAGCCTGGTGTATTTTCCCCACCCAC
CTCAGCAGTTTTCAGCCAGCAGGGACTGATCAGGTGTGTCTCTGGAGTGGGAGCAGAAGGCGTGGCTGGCAAGA
GTGGCCTGGAGAAAGAGGTTTCAGCGCTTGACCAGCCGAGCTGCCCGTACTACAAGATCCAGAACCATGGGCATC
GGGTGAGGTGGGGGGGCACAGGTGTCTATGTGCACCTTCTTGTCTCAGCAAGAAGAGCTGAGAGAGGGGATCTTGG
AGCCATTGAGGGTGTCTATGGAGCTACAGAGGGGAGGGAAAGGTATTTTAAGGTAACAGTGTGGCACAATAGTTAA
GAGCACAGTTTTTGGAGCTAGACCGACATAGGTTCAAATTCTCTTCTGTTGCTTCTTAGTTCTGTAGCCCCAGGT
AAGGGAGTGACTTAACCTCTCTGGACTTCAATTTCTCATCACTAAAGTAGGGCCAATAATAGCACCCACCTCAT
AGGGAAGATTAAATGACATAATGTATGTATGATGCACTAGCAAAGTACCAGTCCCATAGTAAGTCATGCCCCACAG
TATTTCCACCCACCCCTGTTCTCTGCCTTCCCAACCAGGTACTGCAACGACTGGAGCAGAGGCGGCAGCAGGCTT
CAGAGCGGGAGGCTCCAAGCATAGAACAGAGGTTACAGGAAGTGCAGAGAGCATCCGCCGGGCACAGGTGAGCC
AGGTGAAGGGGGCTGCCCGCTGGCCCTGCTGCAGGGGGCTGGCTTAGATGTGGAGCGCTGGCTGAAGCCAGCCA
TGACCCAGGCCCAGGATGAGGTGGAGCAGGAGCGGCGGCTCAGTGAGGCTCGGCTGTCCCAGAGGGACCTCTCTC
CAACCGCTGAGGATGCTGAGCTTTCTGACTTTGAGGAATGTGAGGAGACGGGAGAGCTCTTTGAGGAGCTGCCC
CCCAAGCCCTGGCCACGAGGGCCCTCCCTGCCCTGCACACGTGGTATTTCTGCTATCAGGCAGGGCGTGAGGATG
AGCTGACAATCACGGAGGGTGAGTGGCTGGAGGTATAGAGGAGGGAGATGCTGACGAATGGGTCAAGGCTCGGA
ACCAGCACGGCGAGGTAGGCTTTGTCCCTGAGCGATATCTCAACTTCCCGGACCTCTCCCTCCCAGAGAGCAGCC
AAGACAGTGACAATCCCTGCGGGGCAGAGCCACAGCATTCCTGGCACAGGCCCCTGTACAGCTACACCGGACAGA
GTGCAGAGGAGCTGAGCTTCCCTGAGGGGGCACTCATCCGTCTGCTGCCCCGGGCCCCAAGATGGAGTAGATGACG
GCTTCTGGAGGGGAGAATTTGGGGGCGGTGTTGGGGTCTTCCCCTCCCTGCTGGTGGAAAGAGCTGCTTGGCCCCC
CAGGGCCACCTGAACCTCTCTGACCTGAACAGATGCTGCCGTCCCCTTCTCCTCCCAGCTTCTCCCCACCTGCAC
CTACCTCTGTGTTGGATGGGCCCCCTGCACCTGTCTGCTGGGGACAAAGCCCTGGACTTCCCTGGGTTCTTG
ACATGATGGCACCTCGACTCAGGCCGATGCGTCCACCACCTCCCCCGCCGGCTAAAGCCCCGGATCCTGGCCACC
CAGATCCCCCTACCTTGAAGGCCAGGGAAGCCTTGACCCCCAGTGATGCTGCTGTCCCTATCTTCAAGCTGTGAGA
CCACACCATCAATGATCCAGAGCAACACAGCCAAAAGCTGGAATCGCCCTATTTCCACCCCTCACCTCCAAGGGT
GGAAACTTGGCCCTTCCCATTCTTAGAGCTGGAACCCACTCCTTTTTTTCCCATTTGTTCTATCATCTCTAGGACC
GGAACACTACCTTCTCTTCTGTCTATGACCTATCTAGGGTGGTGAATGCTGAAATCTCTGGGGCTGGAAACC
ATCCATCAAGGTCTCTAGTAGTTCTGGCCACCTCTTTCCCCACCCCTGGCTCCATGACCCACCCACTCTGGATG
CCAGGGTCACTGGGGTTGGGCTGGGAGAGGAACAGGCCTTGGGAATCAGGAGCTGGAGCCAGGATGCGAAGCAG
CTGTAATGGTCTGAGCGGATTTATTGACAATGAATAAAGGGCACGAAGGCCAGGCCAGGGCCTGGGCTCTTGTG
CTAAGAGGGCAGGGGGCCTACGGTGTCTATTGCTTTAGGGGCCACCACGGGCAGGGGCCTGCTCCCAGCTGCCAC
GCTCTATCATATGGAGCGAGGTGTTGGGGAAGGCGGGGCAGGCAGCCTGTTGCAGGCAGGGGAAGGAGAAGAC
TGAGGGGCTGTGACCTCTCCTGAGGCCCCAGCCTGAGACTGTGCAACTCCAGGTGGAAGTAGAGCTGGTCCCTC
AGCTGGGGGGCAGTGCTGTCCAGTGGAGGGGAGGGCTTTACGCCCCACCCACCCCTGGCCCTGCCAGCTGGTAG
TCCATCAGCACAAATGAAGGAGACTTGGAGAAGAGGAAGAATAACACTGTTGCTTCTGTTCAAGCTGTGTCCAGC
TTTTCCCCCTGGGGCTCCAGGACCTTCCCTACCTCCACCACCAAAACCAAGGGATTATAGCAAAGGCTAAGCCTGC
AGTTTACTCTGGGGGTTTCAGGGAGCCGAAAGGCTTAAATAGTTTAAAGTAGGTGATGGGAAGATGAGATTACCTCA
TTTAGGGCTCAGGCAGACTCACCTCACATACTCCCTGCTCCCTGTGGTAGAGACACCTGAGAGAAAGGGAGGGG
TCAACAATGAGAGACCAGGAGTAGGTCTATCAGTGCCCCCAGAGTAGAGAGCAATAAGAGCCAGCCAGTGC
AGTCCCGGCTGTGTTTTCTACCTGGTGATCAGAAGTGTCTGGTTTGGCTGGCTGCCATTTGCCTCTTGAGTGG
GCAGCCCTGGGCTTGGGCCCCCTCCCTCCGGCCCTCAGTGTTGGCTCTGCAGAAGCTCTGGGGTTCCCTTCAAGTG
CACGAGGGGTTAGGCTGCTGTCCCTGAGTCTCCATTCTGTACTGGGGGGCTGGCTAGGACCTGGGGCTGTGGCC
TCTCAGGGGGCAGCCTCTCCATGGCAGGCATCCCTGCCCTGGGCTGCCCTCCCCAGACCCCTGACCAACCCCTG
GGTCTGTCCCCCACCAGAGCCCCAGCTCCTGTCTGTGGGGGAGCCATCACGGTGTTCGTGCAGTCCATAGCGCT
TCTCAATGTGTGTACCCGGAACCTGGGAGGGGAGGGAACACTGGGGTTTAGGACCACAACCTCAGAGGCTGCTTG
GCCCTCCCCCTCTGACCAGGGACATCCTGAGTTTGGTGGCTACTTCCCTCTGGCCTAAGGTAGGGGAGGCGCTTCTC
AGATTGTGGGGCACATTGTGTAGCCTGACTTCTGCTGGAGCTCCAGTCCAGGAGGAAGAGCCAAGGCCCACTT
TTGGGATCAGGTGCCTGATCACTGGGCCCCCTACCTCAGCCCCCTTTCCCTGGAGCACCTGCCCCACCTGCCCA
CAGAGAACACAGTGGTCTCCCCTGTCCGGGGGCGGCTTTTCTTCTTGGAGCGTCCCTGACGGACAAGTGGAG
GCCTCTTGCTGCGGCTGCAATGGATGCAAGGGGCTGCAGAGCCAGGTGCACTGTGTGATGATGGGAGGGGGCTC
CGTCTGCAGGCTGGAGGTGGCATCCACACTGGACAGCAGGAGGAGGGGAGTGAGGGTAACATTTCCATTTCCCT
TCATGTTTTGTTTCTTACGTTCTTTAGCATGCTCCTTAAAACCCAGAGCCCAATTTCCCCAAGCCCCATTT
TTTCTTGCTTTTATCTAATAAACTCAATATTAAG

FIGURE 178

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401

><subunit 1 of 1, 370 aa, 1 stop

><MW: 40685, pI: 4.53, NX(S/T): 0

MQLAKYQSHSKSCPTVFPPTFVLCLPNQVLQRLEQRRQQASEREAPSIEQRLQEVRESIRRA
QVSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPTAEDAELS
DFEECEETGELFEPPAPQALATRALPCPAHVVFQAGREDELTITEGEWLEVIEEGDADEW
VKARNQHGEVGFVPERYLNFPDLSLPRESSQSDNPGAEPTAFLAQALYSYTGQSAEELSFP
EGALIRLLPRAQDGVDDGFWRGEFGGRVGVFPSSLVEELLGPPGPPPELSDPEQMLPSPSPPS
FSPPAPTSVLDGPPAPVLPQDKALDFPGFLDMMAPRLRPMRPPPPPPAKAPDPGHPDPLT

180/249

CACAGGGAGACCCACAGACACATATGCACGAGAGAGACAGAGGAGGAAAGAGACAGAGACAAAGGCACAGCGGAA
GAAGGCAGAGACAGGGCAGGCACAGAAAGCGGCCACAGAGACTCCTACAGAGGGAGAGGCCAGAGAAGCTGCAGA
AGACACAGGCAGGGAGAGACAAAGATCAGGAAAGAGAGGGCTCAGGAGGAGAGTTTGGAGAAAGCAGACCCCTGG
GCACCTCTCCCCAAGCCAAAGACTAAGTTTCTCCATTTCCTTTAACGGTCCTCAGCCCTTCTGAAAACCTTGGCC
TCTGACCTTGGCAGGAGTCCAAGCCCCAGGCTACAGAGAGGAGCTTTCCAAGCTAGGGTGTGGAGGACTTTGGT
GCCCTAGACGGCCTCAGTCCCTCCCAGCTGCAGTACCAGTGCCATGTCCTCCAGACAGGCTCGCATCCCGGGAGGGG
CTTGGCAGGGCGCTGGCTGTGGGGAGCCCAACCTGCTCCTGCTCCCATTTGTGCCGCTCTCCTGGCTGGTGTG
GCTGCTTCTGCTACTGCTGGCTCTCTCCTGCCCTCAGCCCGGCTGGCCAGCCCCCTCCCCCGGAGGAGGAGAT
CGTGTTTCCAGAGAAGCTCAACGGCAGCGTCTCGCTGGCTCGGGCGCCCCCTGCCAGGCTGTTGTGCCGCTTTGCA
GGCTTTTGGGAGACGCTGCTACTAGAGCTGGAGCAGGACTCCGGTGTGAGGTCGAGGGCTGACAGTGCAGT
CCTGGGCGAGGCGCTGAGCTGCTGGGTGGAGCAGAGCTGGCAGCTTACCTGACTGCTGGCACCATCAATGGAGATCC
GGAGTCGGTGGCATCTCTGCACTGGGATGGGGGAGCCCTGTTAGGCGTGTTACAATATCGGGGGGCTGAACTCCA
CCTCCAGCCCCCTGGAGGGAGGCACCCCTAACTCTGCTGGGGGACCTGGGGCTCACATCCTACGCCGGAAGAGTCC
TGCCAGCGGTCAAGGTCCCATGTGCAACGTCAAGGCTCCTCTTGGAAGCCCCAGCCCCAGACCCCCGAAGAGCCAA
GCGCTTTGCTTCACTGAGTAGATTTGTGGAGACACTGGTGGTGGCAGATGACAAGATGGCCGCGATTCACCGGTGC
GGGCTTAAAGCGTACTCTTAACAGTGATGGCAGCAGCAGCCAAAGCCCTCAAGCACCCAAGCATCCGCAATCC
TGTACGCTTGGTGGTGACTCGCTAGTGATCTCGGGTCAGGCGAGGAGGGGCCCAAGTGGGGCCGAGTCTGC
CCAGACCCCTGCGCAGCTTCTGTGCCTGGCAGCGGGGGCCTCAACACCCCTGAGGACTCGGGCCCTGACCACTTTGA
CACAGCCATTTCTGTTTACCCGTGAGACCTGTGTGGAGTCTCCACTTGCACACGCTGGGTATGGCTGATGTGGG
CACCGTCTGTGACCCGGCTCGGAGCTGTGCCATTGTGGAGGATGATGGGCTCCAGTCAGCCCTTCACTGCTGCTCA
TGAATCGGGTCACTGTCTTCAACATGCTCCATGACAACCTCAAGCCATGATCAGTTTGAATGGGCCCTTTGAGCAC
TCTCGCCATGTATGTCGGCCCTGTATGGCTCATGTGGATCTTGAAGAGCCCTGGTCCCCCTCGAGTGGCCGCTT
CATCACTGACTTCTTGGCAATGGCTATGGGCATGTCTCTTAGACAAACCAGAGGCTCCATTGCATCTGCCTGT
GACTTTCCCTGGCAAGGACTATGATGCTGACCGCCAGTGCCAGCTGACCTTCGGGCCCGACTCACGCCATTGTCC
ACAGCTGCCGCGCGCCCTGTGCTGCCCTCTGGTGCTCTGGCCACCTCAATGGCCATGCCATGTGCCAGACCAAACA
CTCGCCCTGGGCGGATGGCACACCCCTGCGGGCCCGCACAGGCCCTGCATGGTGGTTCGCTGCCCTCCACATGGACCA
GCTCCAGGACTTCAATATTCACAGGCTGGTGGCTGGGTCCTTGGGACCATGGGCTGACTGCTCTCGGACCTG
TGGGGTGGTGTCCAGTCTCTCCTCCCGAGACTGCACAGGCTGTGCCCCGGAATGGTGGCAAGTACTGTGAGGG
CCGCGGTACCCGCTTCCGCTCCTGCAACACTGAGGACTGCCCCAAGTGGCTCAGCCCTGACCTTCCGCGAGGAGCA
GTGTGCTGCCACAAACCACCGCACCAGCTCTTCAAGAGCTTCCAGGGGCCATGGACTGGGTTCCTCGCTACAC
AGGCGTGGCCCCCAGGACCAGTGCAAACCTCACCTGCCAGGCCCGGGCAGTGGGCTACTACTATGCTGCTGGAGCC
ACGGTGGTGTAGATGGGACCCCTGTCTCCCCGGACAGCTCCTCGTGTGTGTCAGGGCCGATGACATCCATGCTGG
CTGTGATCGCATCATTTGGCTCCAAGAAAGAGTTTGACAAGTGCGATGGTGTGCGGAGGGGACGGTTCTGGTTGCAG
CAAGCAGTCAGGCTCCTTCAGGAAATTCAGGTACGGATACAACAATGTGGTCACTATCCCCGCGGGGGCCACCCA
CATTTCTTGTCCGGCAGCAGGGAACCCCTGGCCACCGGAGCATCTACTTGGCCCTGAAGCTGCCAGATGGCTCCTA
TGCCCTCAATGGTGAATACACGCTGATGCCCTCCCCACAGATGTGGTACTGCCCTGGGGCAGTCAGCTTGCCTA
CAGCGGGGCCATCGCAGCCTCAGAGACACTGTCAGGCCATGGGCCAGCTGGCCCCAGCTTTGACACTGCAAGTCTT
AGTGGCTGGCAACCCAGGACACAGCCTCCGATACAGCTTCTCGTCCCCGGCCGACCCCTCAACAGCCAC
CCCCACTCCCCAGGACTGGCTGCACCGAAGAGACAGATTTCTGGAGATCCTTCGGCGCGCCCCCTGGGCGGGCAG
GAAAATAACCTCACTATCCCGGCTGCCCTTTCTGGGCACCGGGGCCCTCGGACTTAGCTGGGAGAAAGAGAGAGCTT
CTGTTGCTGCCCTCATGCTAAGACTCAGTGGGGAGGGGCTGTGGGCGTGAGACCTGCCCTCCTCTGCCCTAAT
GCGCAGGCTGGCCCTGCCCTGGTTTCTGCCCTGGGAGGCAGTGATGGGTAGTGGATGGAAGGGGCTGACAGAC
AGCCCTCCATCTAAACTGCCCTCTGCCCCGCGGGTACAGGAGGGAGGGGGAAGGCAGGGGAGGGCCCTGGGCC
CAGTTGACTATTTTATTTATTTATTTATTTATTTATTTAGCACCAGGACGGGGAAGGACTAGGGTCTGGGGAA
CCTTGACCTTATACCCCTCATAGCCCTCACCTTGGGGCTAGGAAATCAAGGGTGATGGTGATAGGTATAAGTGGTG
TGTGTATGCGTGTGTGTGTGTGTGTGAAATGTGTGTGTGTGCTTATGTATGAGGTACAACCTGTTCTGCTTTTCTC
TTCCTGAATTTTATTTTTTGGGAAAAGAAAAGTCAAGGGTAGGGTGGGCCTTCAGGGAGTGAGGGATTATCTTTT
TTTTTTTTTCTTTCTTTCTTTCTTTTCTTTTGTGAGACAGAATCTCGCTCTGTGCCCCAGGCTGGAGTGCAATG
GCACAAATCTCGGCTCACTGCTCCTCCGCTCCCGGCTCAAGTGATTTCTATGCTCAGCCTCCTGAGTAGCTG
GGATACAGGCTCCTGCCACCACGCCACGCTAATTTTTGTTTTGTTTTGTTTTGGAGACAGAGTCTCGCTATTGTC
ACCAGGGCTGGAATGATTTTCAAGCTCACTGCAACCTTCGCCACCTGGGTTCAGCAATTTCTCCTGCCTCAGCCTCC
CGAGTAGCTGAGATTATAGGCACCTACCACCACGCCCGGCTAATTTTTGTATTTTTTAGTAGAGACGGGTTTTAC
CATGTTGGCCAGGCTGGTCTGAACTCCTGACCTTAGGTGATCCACTCGCCTTCATCTCCCAAAGTGCTGGGATT
ACAGGCGTGAGCCACCGTGCTTGGCCACGCCCAACTAATTTTTGTATTTTTTAGTAGAGACAGGGTTTTACCATGT
TGGCAGGCTGCTCTTGAATCCTGACCTCAGGTAATCGACCTGACTTCCGCTGCCAAGTGCTGGGATTACAGG
TGTGAGCCACCACGCCCGGTACATTTTTTAATTAATTAATTTACTATTATTTGATGATCCTTTTGGAGTCAGAC

FIGURE 179B

ATGTGGTTGCATCCTAACTCCATGTCTCTGAGCATTAGATTTCTCATTTGCCAATAATAATACCTCCCTTAGAAG
TTTGTGTGAGGATTAAATAATGTAAATAAAGAACTAGCATAACACTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAGGAAA

FIGURE 180

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492

><subunit 1 of 1, 837 aa, 1 stop

><MW: 90167, pI: 8.39, NX(S/T): 1

MSQTGSHPGRGLAGRWLWGAQPCLLLPVPLSWLVWLLLLLLASLLPSARLASPLPREEEIV
 FPEKLNGSVLPGSGAPARLLCRLQAFGETLLLELEQDSGVQVEGLTVQYLGQAPELLGGAEP
 GTYLTGTINGDPESVASLHWDGGALLGVLYRGAELHLQPLEGGTPNSAGGPGAHILRRKSP
 ASGQGPMCNVKAPLGSPSPRRRAKRFASLSRFVETLVVADDKMAAFHGAGLKRYLLTVMAA
 AAKAFKHPSIRNPVSLVVTRLVILGSGEEGPQVGPSAAQTLRSFCAWQRLNTPEDSGPDHF
 DTAILFTRQDLGCVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAHELGHVFNMLHD
 NSKPCISLNGPLSTSRHVMAVMAHVDPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHL
 PVTFFPGKDYDADRQCQLTFGPDSRHCPQLPPCAALWCSGHLNGHAMCQTKHSPWADGTPCG
 PAQACMGGRCCLHMDQLQDFNIPQAGGWGPWGPWGDCSRTC GGGVQFSSRDCTRVPVRNGGKY
 CEGRRTRFRSCNTEDCPTGSALTFREEQCAAYNHRTDLFKSFPGPMDWVPRYTGAVPQDQCK
 LTCQARALGYYYVLEPRVVDGTPCSPDSSSVCVQGRCIHAGCDRIIGSKKKFDKCMVCGGDG
 SGCSKQSGSFRKFRYGYNVVTIPAGATHILVRQQGNPGRHSIYLALKLPDGSYALNGEYTL
 MPSPTDVVLPGAVSLRYSGATAASETLSGHGPLAQPLTLQVLVAGNPQDTRLRYSFFVPRPT
 PSTPRPTPQDWLHRRRAQILEILRRRPWAGRK

Important features of the protein:

Signal peptide:

amino acids 1-48

N-glycosylation site.

amino acids 68-71

Glycosaminoglycan attachment site

amino acids 188-191, 772-775

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 182-185

Tyrosine kinase phosphorylation site.

amino acids 730-736

N-myristoylation sites.

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-
 172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-
 582, 679-684, 682-687, 763-768

Amidation sites.

amino acids 560-563, 834-837

Leucine zipper pattern.

amino acids 17-38, 24-45

Neutral zinc metalloproteinases, zinc-binding region signature.

amino acids 358-367

FIGURE 181

CAGCAGTGGTCTCTCAGTCTCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACC**ATG**
CAAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCC
AAGAAAATATGTAAATCACTTAAGATTTGTGGACTGGTGTTTGGTATCCTGGCCCTAACTCT
AATTGTCCTGTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAAGCCTATGAC
TGGAGCACACTTTCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAAATTGATCCTGTG
ACCAGAACTGAAATATTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTT
TAAAACGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGA
TTAAAGTGATTCTCTGAATTTTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACC
ACAACTTTCTTTGAACAGTCAGTGATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGA
TTTTCTTAAAAATTCCAAAATTCTGGAGATTTGTGATAACGTGACCATGTATTGGATCAATC
CCACTCTAATATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGGAGAAGATCTTCACTTT
CCTGCCAACGAAAAAAAAGGGATTGAACAAAATGAACAGTGGGTGGTCCCTCAAGTGAAAGT
AGAGAAGACCCGTCACGCCAGACAAGCAAGTGAGGAAGAACTTCCAATAAATGACTATACTG
AAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAGGTTATTGTTGTATTTACTGCCGT
CGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTAGGCTACTACCCATATCCATA
CTGCTACCAAGGAGGACGAGTCATCTGTCGTGTCATCATGCCTTGTAACCTGGTGGGTGGCC
GCATGCTGGGGAGGGTCT**TAA**TAGGAGGTTTGAGCTCAAATGCTTAAACTGCTGGCAACATAT
AATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCCTGGTAGCCAGCT
CTCCAGAATTACTTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACATTATCACC
AAAAAAAAAAAAAAAAAAAAA

FIGURE 182

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727

><subunit 1 of 1, 317 aa, 1 stop

><MW: 37130, pI: 5.18, NX(S/T): 3

MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPPKAY
DMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLVHDFKNGYTGIIYFVGLQKCFIKT
QIKVIPEFSEPEEEIDENEEITTTFFEQSVIWPVPAEKPIENRDFLKNKILEICDNVTMYWI
NPTLISVSELQDFEEEGEDLHFPA NEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDY
TENGIEFDPMLDERGYCCIIYCRGNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWV
ARMLGRV

Important features of the protein:**Signal peptide:**

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

N-myristoylation sites.

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signature.

amino acids 9-14

FIGURE 183

GCGGAACCTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCCGAGGGCCCAGGGAGCTGCC
CGGCTGGCCTAGGCAGGCAGCCGCACC**ATG**GCCAGCACGGCCGTGCAGCTTCTGGGCTTCCT
GCTCAGCTTCCTGGGCATGGTGGGCACGTTGATCACCACCATCCTGCCGCACTGGCGGAGGA
CAGCGCACGTGGGCACCAACATCCTCACGGCCGTGTCCTACCTGAAAGGGCTCTGGATGGAG
TGTGTGTGGCACAGCACAGGCATCTACCAGTGCCAGATCTACCGATCCCTGCTGGCGCTGCC
CCAAGACCTCCAGGCTGCCCCGCGCCCTCATGGTCATCTCCTGCCTGCTCTCGGGCATAGCCT
GCGCCTGCGCCGTATCGGGATGAAGTGACGCGCTGCGCCAAGGGCACACCCGCCAAGACC
ACCTTTGCCATCCTCGGCGGCACCCCTCTTCATCCTGGCCGGCCTCCTGTGCATGGTGGCCGT
CTCCTGGACCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCCAGCGGCATGA
AGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTGGT
GGCACCCTGCTTTGCCTGTCCTGCCAGGACGAGGCACCCTACAGGCCCTACCAGGCCCCGCC
CAGGGCCACCACGACCACTGCAAACACCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAG
ACAATCGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTG
TGAGTCCCCACAGCCTGCTTCTCCCCTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTC
AATGGAGGCAGGGGTTCCAGCACAAAGTTTACTTCTGGGCAATTTTTGTATCCAAGGAAATA
ATGTGAATGCGAGGAAATGTCTTTAGAGCACAGGGACAGAGGGGGAAATAAGAGGAGGAGAA
AGCTCTCTATACCAAAGACTGAAAAAAAAAATCCTGTCTGTTTTTGTATTTATTATATATAT
TTATGTGGGTGATTTGATAACAAGTTTAATATAAAGTGAAGTTGGGAGTTTGGTCAGTGGGGT
TGGTTTGTGATCCAGGAATAAACCTTGCGGATGTGGCTGTTTATGAAAAAAAAAAAAA

FIGURE 184

MASTAVQLLGFLLSFLGMVGTLLITTLPHWRRTAHVGTNILTAVSYLKGLWMECVVHSTGIY
QCQIYRSLLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAKGTPAKTTFAILGGTL
FILAGLLCMVAVSWTTNDVVQNFYNPLLPSGMKFEIGQALYLGFISSSLSLIGGTLLCLSCQ
DEAPYRPYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGYRLNDYV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-103, 115-141, 160-182

187/249

FIGURE 185

GAGCTCCCCCTCAGGAGCGGCTTAGCTTCACACCTTCGGGCAGCAGGAGGGCGGGCAGCTTCTCTC
CAGGCGGCAGGGCGGGCGGCCAGGATC**ATG**TCCACCACCACATGCCAAGTGGTGGCGTTCCT
CCTGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCC
AGGACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGC
GTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCCCTATTTACCATCCTGGGACTTCCAGC
CATGCTGCAGGCAGTGCAGGCCCTGATGATCGTAGGCATCGTCCTGGGTGCCATTGGCCTCC
TGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCC
AACATGACACTGACCTCCGGGATCATGTTTCATTGTCTCAGGTCTTTGTGCAATTGCTGGAGT
GTCTGTGTTTGCCAACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCG
GCATGGGTGGGATGGTGCAGACTGTTACAGACCAGGTACACATTTGGTGCGGCTCTGTTTCGTG
GGCTGGGTCGCTGGAGGCCTCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGG
CCTGGCACCAGAAGAAACCAACTACAAAGCCGTTTCTTATCATGCCTCAGGCCACAGTGTTG
CCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCAACACCAAAAACAAGAAG
ATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATCCTTCCAAGCACGACTA
TGTG**TAA**TGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCACCCAAAA
AACAGGAGATCCCATCTAGATTTCTTCTTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGC
CTCGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCC
ACCATAAAACAGCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTAT
TTCTTTTTTTTAAATATAACTTTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCTCAC
ATTTTGATGATTTAGACAGACTCCCCCTCTTCCTCCTAGTCAATAAACCCATTGATGATCTA
TTTCCCAGCTTATCCCCAAGAAAACTTTTGAAAGGAAAGAGTAGACCCAAAGATGTTATTTT
CTGCTGTTTGAATTTTGTCTCCCCACCCCCAACTTGGCTAGTAATAAACACTTACTGAAGAA
GAAGCAATAAGAGAAAGATATTTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTTACACTG
TGATCTTAAAAGTTACCAAACCAAAGTCATTTTCAGTTTGAGGCAACCAAACCTTTCTACTG
CTGTTGACATCTTCTTATTACAGCAACACCATTCTAGGAGTTTCCTGAGCTCTCCACTGGAG
TCCTCTTTCTGTGCGGGTCAGAAATTGTCCCTAGATGAATGAGAAAATTATTTTTTTTAAAT
TTAAGTCCTAAATATAGTTAAATAAAATAATGTTTTAGTAAATGATACACTATCTCTGTGA
AATAGCCTCACCCCTACATGTGGATAGAAGGAAATGAAAAAATAATTGCTTTGACATTGTCT
ATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATTCATGAAAAGCTCACACCTGTAATC
CTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCCAGAAGTTCGAGACTAGCCTG
GGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAAATCAGCCAGTCATGGTG
GCATACACCTGTAGTCCCAGCATTCGCGGAGGCTGAGGTGGGAGGATCACTTGAGCCCAGGG
AGGTTGGGGCTGCAGTGAGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCGAGA
TCCTGTCTAAAAAAATAAAAAATAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAAA
ACTAATTCTTTAA

FIGURE 186

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734

><subunit 1 of 1, 261 aa, 1 stop

><MW: 27856, pI: 8.50, NX(S/T): 1

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVRQSSGFTE
CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIM
FIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTL
IGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTE
DEVQSYPSKHDYV

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

FIGURE 187

GGAAAACTGTTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCG
GAGTCCAGCTGGCTAAAACTCATCCCAGAGGATA**ATG**GCAACCCATGCCTTAGAAATCGCTG
GGCTGTTTCTTGGTGGTGTGGAATGGTGGGCACAGTGGCTGTCACTGTCATGCCTCAGTGG
AGAGTGTGGCCTTCATTGAAAACAACATCGTGGTTTTTTGAAAACCTCTGGGAAGGACTGTG
GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGG
CTCTTTCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCCTTC
TTGGCTTTTCATGATGGCCATCCTTGGCATGAAATGCACCAGGTGCACGGGGGACAATGAGAA
GGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGC
TCATCCCTGTGAGCTGGGTGGCCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAAT
GTTGCCCCAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGCT
GATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTTGTTGCAACGAAAAGAGCAGTAGCTACA
GATACTCGATACCTTCCCATCGCACAAACCAAAAAAGTTATCACACCGGAAAGAAGTCACCG
AGCGTCTACTCCAGAAGTCAGTATGT**TAG**TTGTGTATGTTTTTTAACTTTACTATAAAGC
CATGCAATGACAAAAATCTATATTACTTTCTCAAATGGACCCCAAGAACTTTGATTTA
CTGTTCTTAAGTGCCTAATCTTAATTACAGGAAGTGTGCATCAGCTATTTATGATTCTATAA
GCTATTTTCAGCAGAATGAGATATTAAACCCAATGCTTTGATTGTTCTAGAAAGTATAGTAAT
TTGTTTTCTAAGGTGGTTCAAGCATCTACTCTTTTTATCATTTACTTCAAATGACATTGCT
AAAGACTGCATTATTTTACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAG
TGTAACATTTATATCTCACATAGAGACATGCTTATATGGTTTTATTTAAAATGAAATGCCAG
TCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAAATCATGGATAGGGTTG
AAGAAGGTTACTATTAATTGTTTTAAAACAGCTTAGGGATTAATGTCCTCCATTTATAATGA
AGATTAAAATGAAGGCTTTAATCAGCATTGTAAAGGAAATTGAATGGCTTTCTGATATGCTG
TTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTTCTCCAGAGGCTTTTTTT
TTCTTGTTATTAAATTAACATTTTTTAAAACGCAGATATTTTGTCAAGGGGCTTTCATTCA
AACTGCTTTTCCAGGGCTATACTCAGAAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATG
GTTTTAGGAAAGTGAAAATATTTTTGTTTTGTATTTGAAGAAGAATGATGCATTTTGACAA
GAAATCATATATGTATGGATATATTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATC
AATATAAATAAAAAGAGCAGAAAAATATGTCTTGGTTTTTCATTTGCTTACCAAAAAACAACA
ACAAAAAAGTTGTCCTTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTCAAAATTG
TCATTTTTGTTCTGTGAAAAATAAATTTCTTCTGTACCATTTCTGTTTAGTTTTACTAAA
ATCTGTAAATACTGTATTTTTCTGTTTATTCCAAATTTGATGAACTGACAATCCAATTTGA
AAGTTTGTGTCGACGTCTGTCTAGCTTAAATGAATGTGTTCTATTTGCTTTATACATTTATA
TTAATAAATTGTACATTTTTCTAATT

FIGURE 188

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735

><subunit 1 of 1, 225 aa, 1 stop

><MW: 24845, pI: 9.07, NX(S/T): 0

MATHALEIAGLFLGGVGMVGTVAVTVMPPQWRVSAFIENNIVVFENFWEGLWMNCVRQANIRM
QCKIYDSLALLSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGI
IFIITGMVVLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVF
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

FIGURE 189

TCGCC**ATG**GCCTCTGCCGGAATGCAGATCCTGGGAGTCGTCTTGACACTGCTGGGCTGGGTG
AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTTCATCGGCAACAGCAT
CGTGGTGGCCCAGGTGGTGTGGGAGGGCCTGTGGATGTCCTGCGTGGTGCAGAGCACCGGCC
AGATGCAGTGCAAGGTGTACGACTCACTGCTGGCGCTGCCACAGGACCTGCAGGCTGCACGT
GCCCTCTGTGTCATCGCCCTCCTTGTGGCCCTGTTTCGGCTTGCTGGTCTACCTTGCTGGGGC
CAAGTGTACCACCTGTGTGGAGGAGAAGGATTCCAAGGCCCGCCTGGTGCTCACCTCTGGGA
TTGTCTTTGTCATCTCAGGGGTCTGACGCTAATCCCCGTGTGCTGGACGGCGCATGCCATC
ATCCGGGACTTCTATAACCCCTGGTGGCTGAGGCCCAAAGCGGGAGCTGGGGGCCTCCCT
CTACTTGGGCTGGGCGGCCTCAGGCCTTTTGTGCTGGGTGGGGGGTTGCTGTGCTGCACTT
GCCCCCTCGGGGGGGTCCCAGGGCCCCAGCCATTACATGGCCCGCTACTCAACATCTGCCCCT
GCCATCTCTCGGGGGCCCTCTGAGTACCCTACCAAGAATTACGTCT**TGA**CGTGGAGGGGAATG
GGGGCTCCGCTGGCGCTAGAGCCATCCAGAAGTGGCAGTGCCCAACAGCTTTGGGATGGGTT
CGTACCTTTTGTCTTCTGCCTCCTGCTATTTTTCTTTTACTGAGGATATTTAAATTCATTT
GAAACTGAGCCAAGGTGTTGACTCAGACTCTCACTTAGGCTCTGCTGTTTCTCACCTTGG
ATGATGGAGCCAAAGAGGGGATGCTTTGAGATTCTGGATCTTGACATGCCCATCTTAGAAGC
CAGTCAAGCTATGGAATAATGCGGAGGCTGCTTGCTGTGCTGGCTTTGCAACAAGACAGAC
TGTCCCCAAGAGTTCCTGCTGCTGCTGGGGGCTGGGCTTCCCTAGATGTCAGTGGACAGCTG
CCCCCATCCTACTCAGGTCTCTGGAGCTCCTCTTTCACCCCTGGAAAAACAAATCATCTG
TTAACAAAGGACTGCCACCTCCGGAACCTTCTGACCTCTGTTTCCCTCCGTCCTGATAAGACG
TCCACCCCCCAGGGCCAGGTCCCAGCTATGTAGACCCCCGCCCCACCTCCAACACTGCACC
CTTCTGCCCTGCCCCCCTCGTCTCACCCCTTTACACTCACATTTTTATCAAATAAAGCATG
TTTTGTTAGTGCA

FIGURE 190

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736

><subunit 1 of 1, 220 aa, 1 stop

><MW: 23292, pI: 8.43, NX(S/T): 0

MASAGMQILGVVLTLLGWVNGLVSCALPMWKVTAFIGNSIVVAQVVWEGWLMSCVVQSTGQM
QCKVYDSLLALPQDLQAARALCVIALLLVALFGLLVYLAGAKCTTCVEEKDSKARLVLTSGIV
FVISGVLTLPVCWTAHAIRDFYNPLVAEAQKREL GASLYLGWAASGLLLLGGGLLCCTCP
SGGSQGPPSHYMARYSTSAPAISRGPPSEYPTKNYV

Transmembrane domains:

amino acids 8-30 (type II), 82-102, 121-140, 166-186

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FIGURE 191

GCCAAGGAGAACATCATCAAAGACTTCTCTAGACTCAAAGGCTTCCACGTTCTACATCTTG
AGCATCTTCTACCACTCCGAATTGAACCAGTCTTCAAAGTAAAGGCAATGGCATTATCC
TTGCAAATTGCTGGGCTGGTTCTTGGGTTCCCTTGGCATGGTGGGACTCTTGCCACAACCCT
TCTGCCTCAGTGGTGGAGTATCAGCTTTTGTGGCAGCAACATTATTGTCTTTGAGAGGCTC
TGGGAAGGGCTCTGGATGAATTGCATCCGACAAGCCAGGGTCCGGTTGCAATGCAAGTTCTA
TAGCTCCTTGTTGGCTCTCCCGCCTGCCCTGGAAACAGCCCGGGCCCTCATGTGTGTGGCTG
TTGCTCTCTCCTTGATCGCCCTGCTTATTGGCATCTGTGGCATGAAGCAGGTCCAGTGCACA
GGCTCTAACGAGAGGGCCAAAGCATACCTTCTGGGAACCTCAGGAGTCCTCTTCATCCTGAC
GGGTATCTTCGTTCTGATTCCGGTGAGCTGGACAGCCAATATAATCATCAGAGATTTCTACA
ACCCAGCCATCCACATAGGTCAGAAACGAGAGCTGGGAGCAGCACTTTTCCTTGGCTGGGCA
AGCGCTGCTGTCTCTTCATTGGAGGGGGTCTGCTTTGTGGATTTTGCTGCTGCAACAGAAA
GAAGCAAGGGTACAGATATCCAGTGCCTGGCTACCGTGTGCCACACACAGATAAGCGAAGAA
ATACGACAATGCTTAGTAAGACCTCCACCAGTTATGTCTTAATGCCTCCTTTTGGCTCCAAGT
ATGGACTATGGTCAATGTTTTTTATAAAGTCCTGCTAGAAACTGTAAGTATGTGAGGCAGGA
GAACTTGCTTTATGTCTAGATTTACATTGATACGAAAGTTTCAATTTGTTACTGGTGGTAGG
AATGAAAATGACTTACTTGGACATTCTGACTTCAGGTGTATTAAATGCATTGACTATTGTTG
GACCCAATCGCTGCTCCAATTTTCATATTCTAAATTCAAGTATACCCATAATCATTAGCAAG
TGTACAATGATGGACTACTTATTACTTTTTGACCATCATGTATTATCTGATAAGAATCTAAA
GTTGAAATTGATATTCTATAACAATAAAACATATACCTATTCTA

FIGURE 192

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737

><subunit 1 of 1, 173 aa, 1 stop

><MW: 18938, pI: 9.99, NX(S/T): 1

MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLLIGICGMKQVQCTGSNER
AKAYLLGTSGVLFILTGIFVLIPVSWTANIIIRDFYNPAIHIGQKRELGAALFLGWASAAVL
FIGGGLLCGFCCCNRRKKQGYRYPVPGYRVPHTDKRRNTTMLS KTSTSYV

Important features of the protein:**Transmembrane domains:**

amino acids 31-51, 71-90, 112-133

N-glycosylation site.

amino acids 161-164

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FIGURE 193

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGCATGAAAGATCACTGGGGGT
CTCCTTCTGCTCTGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCC
AAAAAAAGTGGACTGCAGCATTTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCCATCA
CATACCTACCAGTTTGTGGTTCTGACTACATCACCTATGGGAATGAATGTCACTTGTGTACC
GAGAGCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGTTGCTAAATTCTCCA
TGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCCAGGCTCTGACTG
AGTTTCTTTTCAGTTTTACTGATGTTCTGGGTGGGGGACAGAGCCAGATTCAGAGTAATCTTG
ACTGAATGGAGAAAGTTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCAT
TTTTTTTTTAAACACGTCAATAAAAAAATAATCTCCCAGA

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FIGURE 194

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73739

><subunit 1 of 1, 85 aa, 1 stop

><MW: 9232, pI: 7.94, NX(S/T): 0

MKITGGLLLLCTVVYFCSSSEAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGN

ECHLCTESLKSNGRVQFLHDGSC

Signal peptide:

amino acids 1-19

197/249

FIGURE 195

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCTCGCCCTCCTGCTCGCGCCC
CGCCGCC**ATG**GCTGCCTCCCCGCGCGGCCTGCTGTCCTGGCCCTGACCGGGCTGGCGCTGC
TCCTGCTCCTGTGCTGGGGCCCAGGTGGCATAAGTGGAAATAAACTCAAGCTGATGCTTCAA
AAACGAGAAGCACCTGTTCCAATAAGACTAAAGTGGCCGTTGATGAGAATAAAGCCAAAGA
ATTCCTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCCCGAGGTGC
AGCAGTGGTACCAGCAGTTTCTCTACATGGGCTTTGATGAAGCGAAATTTGAAGATGACATC
ACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCA
CTATGATGAAGACTCTGCAATTGGTCCCCGGAGCCCCTACGGCTTTAGGCATGGAGCCAGCG
TCAACTACGATGACTAC**TAA**CCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATTC
TCTTCATGTATCTCCTAATGCCTTACACTACTTGGTTTCTGATTTGCTCTATTTTCAGCAGAT
CTTTTCTACCTACTTTGTGTGATCAAAAAGAAGAGTTAAAACAACACATGTAAATGCCTTT
TGATATTTTCATGGGAATGCCTCTCATTTAAAAATAGAAATAAAGCATTTTGTAAAAAGA

FIGURE 196

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742

><subunit 1 of 1, 148 aa, 1 stop

><MW: 17183, pI: 8.77, NX(S/T): 0

MAASPARPAVLALTGLALLLLLCWGPGGISGNKLLMLQKREAPVPTKTKVAVDENKAKEFL

GSLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRNGHEYYGDDYYQRHYD

EDSAIGPRSPYGFRHGASVNYDDY

Signal peptide:

amino acids 1-30

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FIGURE 197

CGGCTCGAGCCCGCCCGGAAGTGCCCGAGGGGCGCGATGGAGCTGGGGGAGCCGGGCGCTC
GGTAGCGCGGCGGGCAAGGCAGGCGCC**ATG**ACCCTGATTGAAGGGGTGGGTGATGAGGTGAC
CGTCCTTTTCTCGGTGCTTGCCTGCCTTCTGGTGCTGGCCCTTGCCTGGGTCTCAACGCACA
CCGCTGAGGGCGGGGACCCACTGCCCCAGCCGTCAGGGACCCCAACGCCATCCCAGCCCAGC
GCAGCCATGGCAGCTACCGACAGCATGAGAGGGGAGGCCCCAGGGGCAGAGACCCCCAGCCT
GAGACACAGAGGTCAAGCTGCACAGCCAGAGCCCAGCACGGGGTTCACAGCAACACCGCCAG
CCCCGGACTCCCCGCAGGAGCCCCTCGTGCTACGGCTGAAATTCCTCAATGATTCAGAGCAG
GTGGCCAGGGCCTGGCCCCACGACACCATTGGCTCCTTGAAAAGGACCCAGTTTCCCGGCCG
GGAACAGCAGGTGCGACTCATCTACCAAGGGCAGCTGCTAGGCGACGACACCCAGACCCTGG
GCAGCCTTCACCTCCCTCCCAACTGCGTTCTCCACTGCCACGTGTCCACGAGAGTCGGTCCC
CCAAATCCCCCCTGCCCCGCCGGGGTCCGAGCCCCGGCCCCCTCCGGGCTGGAAATCGGCAGCCT
GCTGCTGCCCCCTGCTGCTCCTGCTGTTGCTGCTGCTCTGGTACTGCCAGATCCAGTACCGGC
CCTTCTTTCCCCTGACCGCCACTCTGGGCCTGGCCGGCTTCACCCTGCTCCTCAGTCTCCTG
GCCTTTGCCATGTACCGCCCCG**TAG**TGCCTCCGCGGGCGCTTGGCAGCGTCGCCGGCCCCCTCC
GGACCTTGCTCCCCGCGCCGCGGGGAGCTGCTGCCTGCCCAGGCCCGCCTCTCCGGCCTG
CCTCTTCCCGCTGCCCTGGAGCCCAGCCCTGCGCCGCAGAGGACTCCCGGGACTGGCGGAGG
CCCCGCCCTGCGACCGCCGGGGCTCGGGGCCACCTCCCGGGGCTGCTGAACCTCAGCCCGCA
CTGGGAGTGGGCTCCTCGGGGTGCGGCATCTGCTGTCGCTGCCTCGGCCCCGGGCAGAGCCG
GGCCGCCCCGGGGGCCCCGTCTTAGTGTTCTGCCGGAGGACCCAGCCGCCTCCAATCCCTGAC
AGCTCCTTGGGCTGAGTTGGGGACGCCAGGTCGGTGGGAGGCTGGTGAAGGGGAGCGGGGAG
GGGCAGAGGAGTTCCCCGGAACCCGTGCAGATTAAAGTAACTGTGAAGTTTTAAAAAAAAAA
AAAAAAA

FIGURE 198

MTLIEGVGDEVTVLFSVLACLLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPSAAMAATDSM
RGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVLRKFLNDSEQVARAWPHDT
IGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRVGPPNPPCPPGS
EPGPSGLEIGSLLLPLLLLLLLLLLWYCQIQYRPFPLTATLGLAGFTLLLSLLAFAMYRP

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 195-217

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FIGURE 199

GAGATTGGAAACAGGACAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAG
ATTCCCCAGGCTCTCAGAGAAGATCAGCAGAAAGTCTGCAAGACCCTAAGAACCATCAGCCC
TCAGCTGCACCTCCTCCCCTCCAAGG**ATG**ACAAAGGCGCTACTCATCTATTTGGTCAGCAGC
TTTCTTGCCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTGGCCAGGTGCTGCAGCT
GGAGGACTTGGATGGGTTTGAGGGTTACTCCCTGAGTGACTGGCTGTGCCTGGCTTTTGTGG
AAAGCAAGTTCAACATATCAAAGATAAATGAAAATGCGGATGGAAGCTTTGACTATGGCCTC
TTCCAGATCAACAGCCACTACTGGTGCAACGATTATAAGAGTACTCGGAAAACCTTTGCCA
CGTAGACTGTCAAGATCTGCTGAATCCCAACCTTCTTGCAAGGCATCCACTGCGCAAAAAGGA
TTGTGTCCGGAGCACGGGGGATGAACAACCTGGGTAGAATGGAGGTTGCACTGTTCAGGCCGG
CCACTCTCCTACTGGCTGACAGGATGCCGCCTGAGAT**TGA**AACAGGGTGCGGGTGCACCGTGG
AGTCATTCCAAGACTCCTGTCCTCACTCAGGGATTCTTCATTTCTTCTTCTACTGCCTCCA
CTTCATGTTATTTTCTTCCCTTCCCATTTACAACATAAACTGACCAGAGCCCCAGGAATAAA
TGGTTTTCTTGGCTTCCTCCTTACTCCCATCTGGACCCAGTCCCCTGGTTCCTGTCTGTTAT
TTGTAAACTGAGGACCACAATAAAGAAATCTTTATATTTATCG

FIGURE 200

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746

><subunit 1 of 1, 148 aa, 1 stop

><MW: 16896, pI: 6.05, NX(S/T): 1

MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCCLAFVESKFNISKI

NENADGSFDYGLFQINSHYWCNDYKSYSENLCNVDCQDLLNPNLLAGIHCAKRIVSGARGMN

NWVEWRLHCSGRPLSYWLTGCRLR

Signal peptide:

amino acids 1-18

203/249

TCTGACCTGACTGGAAGCGTCCAAAGAGGAGCGGCTGTGACGCCCTGCTTGACTGAGAACCCA
 CCAGCTCATCCCAGACACCTCATAGCAACCTATTTATACAAAGGGGGAAAGAAACACCTGAG
 CAGAATGGAATCATTTATTTTTTTTCCCAAGGAGAAAACCGGGTAAAGGGAGGGAAGCAATTC
 AATTTGAAGTCCCTGTGAATGGGCTTTCAGAAGGCAATTAAAGAAATCCACTCAGAGAGGAC
 TTGGGGTGAAACTTTGGGTCTGTGGTTTTCTGATTGTAAGTGGAAGCAGGTCTTGCACACGC
 TGTTGGCAAATGTCAGGACCAGGTTAAGTGACTGGCAGAAAACTTCCAGGTGGAACAAGCA
 ACCCATGTTCTGCTGCAAGCTTGAAGGAGCCTGGAGCGGGAGAAAGCTAACTTGAACATGAC
 CTGTTGCATTTGGCAAGTTCTAGCAAC**ATG**CTCCTAAGGAAGCGATACAGGCACAGACCATG
 CAGACTCCAGTTCCCTCCTGCTGCTCCTGATGCTGGGATGCGTCCTGATGATGGTGGCGATGT
 TGCACCCTCCCCACCACACCCTGCACCAGACTGTCACAGCCCAAGCCAGCAAGCACAGCCCT
 GAAGCCAGGTACCGCCTGGACTTTGGGGAATCCCAGGATTGGGTACTGGAAGCTGAGGATGA
 GGGTGAAGAGTACAGCCCTCTGGAGGGCCTGCCACCCTTTATCTCACTGCGGGAGGATCAGC
 TGCTGGTGGCCGTGGCCTTACCCCAGGCCAGAAGGAACCAGAGCCAGGGCAGGAGAGGTGGG
 AGCTACCGCCTCATCAAGCAGCCAAGGAGGCAGGATAAGGAAGCCCCAAAGAGGGACTGGGG
 GGCTGATGAGGACGGGGAGGTGTCTGAAGAAGAGGAGTTGACCCCGTTACGCTGGACCCAC
 GTGGCCTCCAGGAGGCACCTCAGTGCCCCGATCCCCCTCCAGAGGGCTCTGCCCCAGGTGCGG
 CACCCACTGTGTCTGCAGCAGCACCCCTCAGGACAGCCTGCCCACAGCCAGCGTCATCCTCTG
 TTTCCATGATGAGGCCTGGTCCACTCTCCTGCGGACTGTACACAGCATCCTCGACACAGTGC
 CCAGGGCCTTCCCTGAAGGAGATCATCCTCGTGGACGACCTCAGCCAGCAAGGACAACCAAG
 TCTGCTCTCAGCGAATATGTGGCCAGGCTGGAGGGGGTGAAGTTACTCAGGAGCAACAAGAG
 GCTGGGTGCCATCAGGGCCCGGATGCTGGGGGCCACCAGAGCCACCGGGGATGTGCTCGTCT
 TCATGGATGCCCACTGCGAGTGCCACCCAGGCTGGCTGGAGCCCTCCTCAGCAGAATAGCT
 GGTGACAGGAGCCGAGTGGTATCTCCGGTGATAGATGTGATTGACTGGAAGACTTTCCAGTA
 TTACCCCTCAAAGGACCTGCAGCGTGGGGTGTGTGGACTGGAAGCTGGATTTCCACTGGGAAC
 CTTTGCCAGAGCATGTGAGGAAGGCCCTCCAGTCCCCCATAAGCCCCATCAGGAGCCCTGTG
 GTGCCCCGAGAGGTGGTGGCCATGGACAGACATTACTTCCAAACACTGGAGCGTATGACTC
 TCTTATGTCGCTGCGAGGTGGTGAAAACCTCGAACTGTCTTTCAAGGCCTGGCTCTGTGGTG
 GCTCTGTTGAAATCCTTCCCTGCTCTCGGGTAGGACACATCTACCAAATCAGGATTCCCAT
 TCCCCCTCGACCAGGAGGCCACCCTGAGGAACAGGGTTTCGATTGCTGAGACCTGGCTGGG
 GTCATTCAAAGAAACCTTCTACAAGCATAGCCCAGAGGCCTTCTCCTTGAGCAAGGCTGAGA
 AGCCAGACTGCATGGAACGCTTGCAGCTGCAAAGGAGACTGGGTTGTCGGACATTCCACTGG
 TTTCTGGCTAATGTCTACCCTGAGCTGTACCCATCTGAACCCAGGGCCAGATTTCTCTGGAAA
 GCTCCACAACACTGGACTTGGGCTCTGTGCAGACTGCCAGGCAGAAGGGGACATCCTGGGCT
 GTCCCATGGTGTGGCTCCTTGCAGTGACAGCCGGCAGCAACAGTACCTGCAGCACACCAGC
 AGGAAGGAGATTCACTTTGGCAGCCACAGCACCTGTGCTTTGCTGTCAGGCAGGAGCAGGT
 GATTCTTCAGAACTGCACGGAGGAAGGCCTGGCCATCCACCAGCAGCACTGGGACTTCCAGG
 AGAATGGGATGATTGTCCACATTCTTTCTGGGAAATGCATGGAAGCTGTGGTGCAAGAAAAC
 AATAAAGATTTGTACCTGCGTCCGTGTGATGGAAAAGCCCGCCAGCAGTGGCGATTTGACCA
 GATAAATGCTGTGGATGAACGAT**TGA**ATGTCAATGTCAGAAGGAAAAGAGAATTTTGGCCATC
 AAAATCCAGCTCCAAGTGAACGTAAAGAGCTTATATATTTTCATGAAGCTGATCCTTTTGTGT
 GTGTGCTCCTTGTGTTAGGAGAGAAAAAGCTCTATGAAAGAATATAGGAAGTTTCTCCTTT
 TCACACCTTATTTTCATTGACTGCTGGCTGCTTA

FIGURE 202

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760

><subunit 1 of 1, 639 aa, 1 stop

><MW: 73063, pI: 6.84, NX(S/T): 2

MLLRKRYRHRPCRLQFLLLLLLMLGCVLMMVAMLHPPHHTLHQTVTAQASKHSPEARYRLDFG
ESQDWVLEAEDEGEYSPLEGLPPFISLREDQLLVAVALPQARRNQSQGRRGGSYRLIKQPR
RQDKEAPKRWDGADEDEGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHP
QDSLPTASVILCFHDEAWSTLLRTVHSILDTVPRAFLKEIILVDDLSQQGQLKSALSEYVAR
LEGVKLLRSNKRLGAI RARMLGATRATGDVLVFMDAHCECHPGWLEPLLSRIAGDRSRVVSP
VIDVIDWKTFQYYPSKDLQRGVLDWKLDHFHWEPLPEHVRKALQSPISPIRSPVVPGEVVAMD
RHYFQNTGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGHIIYQNQDSHSPLDQEATL
RNRVRIAETWLGSFKETFYKHSPEAFSLSKAEKPDCMERLQLQRRLLGCRTFHWFLANVYPEL
YPSEPRPSFSGKLHNTGLGLCADCQAEGDILGCPMVLAPCSDSRQQQYLQHTSRKEIHFGSP
QHL CFAVRQEQVILQNCTEEGLAIHQQHWDFQENGMIVHILSGKCMEAVVQENNKDLYLRPC
DGKARQQWRFDQINAVDER

Signal peptide:

amino acids 1-28

FIGURE 203

CGCCAAGCATGCAGTAAAGGCTGAAAATCTGGGTACAGCTGAGGAAGACCTCAGAC**ATGGA**
 GTCCAGGATGTGGCCTGCGCTGCTGCTGTCCCACCTCCTCCCTCTCTGGCCACTGCTGTTGC
 TGCCCCCTCCCACCGCTGCTCAGGGCTCTTCATCCTCCCCCTCGAACCCACACAGCCCCAGCC
 CGCCCCCGTGTGCCAGGGGAGGCCCCCTCGGCCCCACGTCTATGTGTGCGTGTGGGAGCGAGC
 ACCTCCACCAAGCCGATCTCCTCGGGTCCCAAGATCACGTGCGCAAGTCCTGCCTGGCACTG
 CACCCCCAGCCACCCCATCAGGCTTTGAGGAGGGGCGGCCCTCATCCCAATACCCCTGGGCT
 ATCGTGTGGGGTCCCACCGTGTCTCGAGAGGATGGAGGGGACCCCAACTCTGCCAATCCCGG
 ATTTCTGGACTATGGTTTTTGAGCCCCCTCATGGGCTCGCAACCCACACCCCAACTCAGACT
 CCATGCGAGGTGATGGAGATGGGCTTATCCTTGAGAGGACCTGCCACCCTGCGGCCATTCTC
 CTGTTCCGGGGGCCGTGGGGAAGGTGTGGACCCCCAGCTCTATGTCACAATTACCATCTCCAT
 CATCATTGTTCTCGTGGCCACTGGCATCATCTTCAAGTTCTGCTGGGACCGCAGCCAGAAGC
 GACGCAGACCCCTCAGGGCAGCAAGGTGCCCTGAGGCAGGAGGAGAGCCAGCAGCCACTGACA
 GACCTGTCCCCGGCTGGAGTCACTGTGCTGGGGGCCCTTCGGGGACTCACCTACCCCCACCCC
 TGACCATGAGGAGCCCCGAGGGGGACCCCGGCCCTGGGATGCCCCACCCCAAGGGGGCTCCAG
 CCTTCCAGTTGAACCGG**TGAG**GGGCAGGGGCAATGGGATGGGAGGGCAAAGAGGGGAAGGCAAC
 TTAGGTCTTCAGAGCTGGGGTGGGGGTGCCCTCTGGATGGGTAGTGAGGAGGCAGGCGTGGC
 CTCCCACAGCCCCCTGGCCCTCCCAAGGGGGCTGGACCAGCTCCTCTCTGGGAGGCACCCTTC
 CTTCTCCCAGTCTCTCAGGATCTGTGTCCTATTCTCTGCTGCCCATAACTCCAACTCTGCCC
 TCTTTGGTTTTTTCTCATGCCACCTTGTCTAAGACAACCTCTGCCCTCTTAACCTTGATTCCC
 CCTCTTTGTCTTGAACCTTCCCCTTCTATTCTGGCCTACCCCTTGTTTCTGACTGTGCCCTT
 TCCCTCTTCTCTCAGGATTCCCCTGGTGAATCTGTGATGCCCCCAATGTTGGGGTGCAGCC
 AAGCAGGAGGCCAAGGGGGCCGGCACAGCCCCCATCCCACTGAGGGTGGGGCAGCTGTGGGGA
 GCTGGGGCCACAGGGGCTCCTGGCTCCTGCCCCCTTGACACACCACCCGGAACACTCCCCAGCC
 CCACGGGCAATCCTATCTGCTCGCCCTCCTGCAGGTGGGGGCCCTCACATATCTGTGACTTCG
 GGTCCCTGTCCCCACCCCTTGTGCACTCACATGAAAGCCTTGACACTCACCTCCACCTTCAC
 AGGCCATTGACACAGCTCCTGCACCCTCTCCCCGTCCATACCGCTCCGCTCAGCTGACTCT
 CATGTTCTCTCGTCTCACATTTGCACTCTCTCCTTCCCACATTCTGTGCTCAGCTCACTCAG
 TGGTCAGCGTTTCTTGCACACTTTACCTCTCATGTGCGTTTCCCGGCCTGATGTTGTGGTGG
 TGTGCGGCGTGTCACTCTCTCCCTCATGAACACCCACCCACCTCGTTTCCGCAGCCCCCTGC
 GTGCTGCTCCAGAGGTGGGTGGGAGGTGAGCTGGGGGCTCCTTGGGGCCCTCATCGGTCTATGG
 TCTCGTCCCATTCACACCAATTTGTTTCTCTGTCTCCCCATCCTACTCCAAGGATGCCGGCA
 TCACCCTGAGGGCTCCCCCTTGGGAATGGGGTAGTGAGGCCCCAGACTTCACCCCCAGCCCA
 CTGCTAAAATCTGTTTTCTGACAGATGGGTTTTGGGGAGTCGCCTGCTGCACTACATGAGAA
 AGGGAATCCCATTTGCCCTTCCCTTCTCCTACAGTCCCTTTTGTCTTGTCTGTCTGGCTG
 TCTGTGTGTGTGCCATTCTCTGGACTTCAGAGCCCCCTGAGCCAGTCCTCCCTTCCCAGCCT
 CCCTTTGGGCCTCCCTAACTCCACCTAGGCTGCCAGGGACCGGAGTCAGCTGGTTCAAGGCC
 ATCGGGAGCTCTGCCTCCAAGTCTACCCTTCCCTTCCCGGACTCCCTCCTGTCCCCCTCCTTT
 CCTCCCTCCTTCCCTTCCACTCTCCTTCCCTTTGCTTCCCTGCCCTTCCCCCTCCTCAGGTT
 CTTCCCTCCTTCTCACTGGTTTTTTCCACCTTCCCTTCCCTTCTTCCCTGGCTCCTAGGCT
 GTGATATATATTTTTGTATTATCTTTTCTTCTTCTTGTGGTGATCATCTTGAATTACTGTG
 GGATGTAAGTTTCAAATTTTCAAATAAAGCCTTTGCAAGATAA

FIGURE 204

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV
PGRDGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAEC SGPLPIEAIYLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

FIGURE 205

GTTAACCAGCGCAGTCCTCCGTGCGTCCCGCCCGCCGCTGCCCTCACTCCCGGCCAGGATGG
CATCCTGTCTGGCCCTGCGCATGGCGCTGCTGCTGGTCTCCGGGGTTCTGGCCCTGCGGTG
CTCACAGACGATGTTCCACAGGAGCCCGTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCC
GTCGGGAGAAGGCCCCGTGGAGAGCACAGCCCCGGCCGGGAGCCCGTGGACACCGGTCCCC
CAGCCCCACCGTCGCGCCAGGACCCGAGGACAGCACCGCGCAGGAGCGGCTGGACCAGGGC
GGCGGGTCGCTGGGGCCCGGCGCTATCGCGGCCATCGTGATCGCCGCCCTGCTGGCCACCTG
CGTGGTGCTGGCGCTCGTGGTCGTCGCGCTGAGAAAGTTTTCTGCCTCCTGAAGCGAATAAA
GGGGCCGCGCCCGGCGGCGCGGCGGCGACTCGGCAAAAAAAAAAAAAA

FIGURE 206

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398

><subunit 1 of 1, 121 aa, 1 stop

><MW: 12073, pI: 4.11, NX(S/T): 0

MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVESTSPGREPVDTG
PPAPTVAPGPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 91-110

Glycosaminoglycan attachment site.

amino acids 44-47

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 116-119

N-myristoylation site.

amino acids 91-96

FIGURE 207

GGCGTTGGTTGGTGGCGGCTGAAGGGTGTGGCGCGAGCAGCGTCTTGGTTGGCCGGCGG
CGGGCCGGGACGGGCATGGCCCTGCTGCTGTGCCTGGTGTGCCTGACGGCGGCGCTGGCCCA
CGGCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGA
ACTTCAAGTCCTGGTGGGTGGGCGACATCCCCGTGTCAGGGGCGCTGCTCACCGACTGGAGC
GACGACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATCACCCGGGAGAAGCTGGA
CCAAGTGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGGAAGATGTACTTCC
CCGGGTATTTCCCCAACGAGCTGCGAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAAC
GCCATCATCGAAAGGCACCTGGCACCAGGCAGCTGGGGAGGAGGGCAGCTCTCAGGGAGGG
ACCCAGCCTAGCACCTGAAGGATCAATGCCATCACCCCGCGGGGACCTCCCCTAAGTAGCCC
CCAGAGGCGCTGGGAGTGTTGCCACCGCCCTCCCCTGAAGTTTGCTCCATCTCACGCTGGGG
GTCAACCTGGGGACCCCTTCCCTCCGGGCCATGGACACACATACATGAAAACCAGGCCGCAT
CGACTGTCAGCACCGCTGTGGCATCTTCCAGTACGAGACCATCTCCTGCAACAACCTGCACAG
ACTCGCACGTGCCTGCTTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCCGT
GCCAGGGCCCTACTGTCCCTGGGGTCCCAGGCTCTCCTTGGAGGGGGCTCCCCGCCTTCCAC
CTGGCTGTCATCGGGTAGGGCGGGGCCGTGGGTTCAGGGGCGCACCACTTCCAAGCCTGTGT
CCCACAGGTCCTCGGCGCAGTGGAAGTCAGCTGTCCAGGGCCTCCTGAACTACATAAATAAC
TGGCACAAGTAAGTCCCCCTCTCAAACCAACACAGGCAGTGTGTGTATGTGAGCACCTCGTG
GGTGAGTATGTGTGGGGCACAGGCTGGCTCCCTCAGCTCCCACGTCTTAGAGGGGGCTCCCGA
GGAGGTGGAACCTCAACCCAGCTCTGCGCAGGAGGCGGCTGCAGTCCTTTTCTCCCTCAAAG
GTCTCCGACCCTCAGCTGGAGGCGGGCATCTTTCCTAAAGGGTCCCCATAGGGTCTGGTTCC
ACCCCATCCCAGGTCTGTGGTCAGAGCCTGGGAGGGTTCCCTACGATGGTTAGGGGTGCCCC
ATGGAGGGGCTGACTGCCCCACATTGCCTTTTACAGACAGGACACGAGCATGAGGTAAGGCCGC
CCTGACCTGGACTTCAGGGGGAGGGGGTAAAGGGAGAGAGGAGGGGGGCTAGGGGGTCTCT
AGATCAGTGGGGGCACTGCAGGTGGGGCTCTCCCTATACCTGGGACACCTGCTGGATGTCAC
CTCTGCAACCACACCCATGTGGTGGTTTCATGAACAGACCACGCTCCTCTGCCTTCTCCTGG
CCTGGGACACACAGAGCCACCCCGGCCTTGTGAGTGACCCAGAGAAGGGAGGCCTCGGGAGA
AGGGGTGCTCGTAAGCCAACACCAGCGTGCCGCGGCCTGCACACCCTTCGGACATCCCAGGC
ACGAGGGTGTCGTGGATGTGGCCACACATAGGACCACACGTCCCAGCTGGGAGGAGAGGCCT
GGGGCCCCCAGGGAGGGAGGCAGGGGGTGGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCC
CCGCAGCCTGGTATCGCCAGCCTTAAGGTGTCTGGAGCCCCCACACTTGGCCAACCTGACCT
TGGAAGATGCTGCTGAGTGTCTCAAGCAGCACTGACAGCAGCTGGGCCTGCCCCAGGGCAAC
GTGGGGGCGGAGACTCAGCTGGACAGCCCCTGCCTGTCACCTCTGGAGCTGGGCTGCTGCTGC
CTCAGGACCCCCTCTCCGACCCCGGACAGAGCTGAGCTGGCCAGGGCCAGGAGGGCGGGAGG
GAGGGAATGGGGGTGGGCTGTGCGCAGCATCAGCGCCTGGGCAGGTCCGCAGAGCTGCGGGA
TGTGATTAAAGTCCCTGATGTTTCTC

FIGURE 208

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399

><subunit 1 of 1, 157 aa, 1 stop

><MW: 17681, pI: 7.65, NX(S/T): 1

MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMK
ELHLAIPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAIIER
HLAPGSWGGGQLSREGPSLAPEGSMPSPRGDLP

Signal peptide:

amino acids 1-15

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FIGURE 209

AGCAGGAGCAGGAGAGGGACAATGGAAAGCTGCCCCGTCCAGGTTTCATGTTCCCTCTTATTTCT
CCTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCCTG
GTGCTGCCCAGGAACCCACGTGGCTCACAGATGTCCAGCTGCCATGGAATTCATTGCTGCC
ACTGAGGTGGCTGTCATAGGCTTCTTCCAGGATTTAGAAATACCAGCAGTGCCCATACTCCA
TAGCATGGTGCAAAAATTCCCAGGCGTGTCATTTGGGATCAGCACTGATTCTGAGGTTCTGA
CACACTACAACATCACTGGGAACACCATCTGCCTCTTTCGCCTGGTAGACAATGAACAACCTG
AATTTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTTCATTGAGAT
CAACAGCCTCCACATGGTGACAGAGTACAACCCTGTGACTGTGATTGGGTTATTCAACAGCG
TAATTCAGATTCATCTCCTCCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAACATG
CACAGATACCAGAAGGCAGCCAAGCTCTTCCAGGGGAAGATTCTCTTTATTCTGGTGGACAG
TGGTATGAAAGAAAATGGGAAGGTGATATCATTTTTTCAAACCTAAAGGAGTCTCAACTGCCAG
CTTTGGCAATTTACCAGACTCTAGATGACGAGTGGGATACACTGCCCCACAGCAGAAGTTTCC
GTAGAGCATGTGCAAACTTTTGTGATGGATTCCCTAAGTGGAAAATTGTTGAAAGAAAATCG
TGAATCAGAAGGAAAGACTCCAAAGGTGGAACCTTGACTTCTCCTTGGAACCTACATATGGCC
AAGTATCTACTTTATGCAAAGTAAAAGGCACAACCTCAAATCTCAGAGACACTAAACAACAG
GATCACTAGGCCTGCCAACCACACACACACGCACGTGCACACACGCACGCACGCGTGCACAC
ACACACGCGCACACACACACACACACAGAGCTTCATTTCCCTGTCTTAAAATCTCGTTTTCTC
TTCTTCCTTCTTTTAAATTTTCATATCCTCACTCCCTATCCAATTTCTTCTTATCGTGCATT
CATACTCTGTAAGCCCATCTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATG
CCTCTATGAAAGAGAGGCATTCCCTAGAGAAAGATTGTTCCAATTTGTCATTTAATATCAAGT
TTGTATACTGCACATGACTTACACACAACATAGTTCCTGCTCTTTTAAGGTTACCTAAGGGT
TGAAACTCTACCTTCTTTCATAAGCACATGTCCGTCTCTGACTCAGGATCAAAAACCAAAGG
ATGGTTTTTAACACCTTTGTGAAATTGTCTTTTTTGCCAGAAGTTAAAGGCTGTCTCCAAGTC
CCTGAACTCAGCAGAAATAGACCATGTGAAAACCTCATGCTTGGTTAGCATCTCCAACCTCCC
TATGTAAATCAACAACCTGCATAATAATAAAAGGCAATCATGTTATA

FIGURE 210

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401

><subunit 1 of 1, 273 aa, 1 stop

><MW: 30480, pI: 4.60, NX(S/T): 1

MEAAPSRFMFLLFLLTCELAAEVAAEVEKSSDGPGAAQEPTWLTDVPAAMEFIAATEVAVIG
FFQDLEIPAVPILHSMVQKFPGVSEFGISTDSEVLTHYNITGNTICLFRLVDNEQLNLEDEDI
ESIDATKLSRFIEINSLHMTVEYNPVTVIGLFNSVIQIHLLIMNKASPEYEENMHRYQKAA
KLFQGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDDEWDTLPTAEVSVEHVQNF
CDGFLSGKLLKENRESEGKTPKVEL

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 143-162

FIGURE 211

GGAGAGCCGCGGCTGGGACCGGAGCTGGAGCGCGGCTGGAGGTGCCACCCGGCGCGGGTG
GCGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGG
GACGCGGCGGCGGCGGCGGCGACTGCAGTGGCTGGACG**ATGG**CAGCGTCCGCCGGAGCCGGG
GCGGTGATTGCAGCCCCAGACAGCCGGCGCTGGCTGTGGTTCGGTGCTGGCGGCGGCGCTTGG
GCTCTTGACAGCTGGAGTATCAGCCTTGGAAGTATATACGCCAAAAGAAATCTTCGTGGCAA
ATGGTACACAAGGGAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACC
TCAGTCTCCTGGAGCTTCCAGCCAGAGGGGGCCGACACTACTGTGTCTGTTTTTCCACTACTC
CCAAGGGCAAGTGTACCTTGGGAATTATCCACCATTTAAAGACAGAATCAGCTGGGCTGGAG
ACCTTGACAAGAAAGATGCATCAATCAACATAGAAAATATGCAGTTTATACACAATGGCACC
TATATCTGTGATGTCAAAAACCTCCTGACATCGTTGTCCAGCCTGGACACATTAGGCTCTA
TGTCGTAGAAAAAGAGAATTTGCCTGTGTTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTG
CTGTGGTCCTAGGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCTCTATAGAAGGAAA
AACTCTAAACGGGATTACACTGGCTGCAGTACATCAGAGAGTTTGTACCAGTTAAGCAGGC
TCCTCGGAAGTCCCCCTCCGACACTGAGGGTCTTGTAAGAGTCTGCCTTCTGGATCTCACC
AGGGCCCAAGTCATATATGCACAGTTAGACCACTCCGGCGGACATCACAGTGACAAGATTAAC
AAGTCAGAGTCTGTGGTGTATGCGGATATCCGAAAGAAT**TAA**GAGAATACCTAGAACATATC
CTCAGCAAGAAACAAAACCAAACCTGGACTCTCGTGCAGAAAATGTAGCCCATTACCACATGT
AGCCTTGGAGACCCAGGCAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAGATGTGT
ACAAAGGATATGTATAAATATTCTATTTAGTCATCCTGATATGAGGAGCCAGTGTTGCATGA
TGAAAAGATGGTATGATTCTACATATGTACCCATTGTCTTGCTGTTTTTGTACTTTCTTTTC
AGGTCATTTACAATTGGGAGATTTTCAGAAACATTCCTTTCACCATCATTTAGAAATGGTTTG
CCTTAATGGAGACAATAGCAGATCCTGTAGTATTTCCAGTAGACATGGCCTTTTAATCTAAG
GGCTTAAGACTGATTAGTCTTAGCATTTACTGTAGTTGGAGGATGGAGATGCTATGATGGAA
GCATACCCAGGGTGGCCTTTAGCACAGTATCAGTACCATTTATTTGTCTGCCGCTTTTAAAA
AATACCCATTGGCTATGCCACTTGAAAACAATTTGAGAAGTTTTTTTTGAAGTTTTTCTCACT
AAAATATGGGGCAATTGTTAGCCTTACATGTTGTGTAGACTTACTTTAAGTTTGCACCCTTG
AAATGTGTCATATCAATTTCTGGATTCAATAAGCAAGATTAGCAAAGGATAAATGCCGAAG
GTCACCTTCATTCTGGACACAGTTGGATCAATACTGATTAAGTAGAAAATCCAAGCTTTGCTT
GAGAACTTTTGTAACTGGAGAGTAAAAAGTATCGGTTTTTA

FIGURE 212

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510

><subunit 1 of 1, 269 aa, 1 stop

><MW: 29082, pI: 9.02, NX(S/T): 3

MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKS
TSTTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDDKKDASINIEN
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVGIVTAVVLGLTLLISMI
LAVLYRRKNSKRDTGCGSTSESLSPVKQAPRKSPDTEGLVKSLPSGSHQGPVIYAQLDHSG
GHHSDKINKSESVVYADIRKN

Signal peptide:

amino acids 1-37

Transmembrane domain:

amino acids 161-183

FIGURE 213

GCCGGCTGTGCAGAGACGCC**ATG**TACCGGCTCCTGTCAGCAGTGACTGCCCGGGCTGCCGCC
 CCCGGGGGCTTGGCCTCAAGCTGCGGACGACGCGGGGTCCATCAGCGCGCCGGGCTGCCGCC
 TCTCGGCCACGGCTGGGTGCGGGGGCCTCGGGCTGGGGCTGGGGCTGGCGCTCGGGGTGAAGC
 TGGCAGGTGGGCTGAGGGGCGCGGCCCGGCGCAGTCCCCCGCGGCCCGGACCCTGAGGCG
 TCGCCTCTGGCCGAGCCGCCACAGGAGCAGTCCCTCGCCCCGTGGTCTCCGCAGACCCCGGC
 GCCGCCCTGCTCCAGGTGCTTCGCCAGAGCCATCGAGAGCAGCCGCGACCTGCTGCACAGGA
 TCAAGGATGAGGTGGGCGCACCGGGGCATAGTGGTTGGAGTTTCTGTAGATGGAAAAGAAGTC
 TGGTCAGAAGGTTTAGGTTATGCTGATGTTGAGAACCGTGTACCATGTAAACCAGAGACAGT
 TATGCGAATTGCTAGCATCAGCAAAAGTCTCACCATGGTTGCTCTTGCCAAATTGTGGGAAG
 CAGGGAAACTGGATCTTGATATTCCAGTACAACATTATGTTCCCGAATTCCAGAAAAAGAA
 TATGAAGGTGAAAAGGTTTCTGTCAACAAGATTACTGATTTCCCATTTAAGTGGAATTCTG
 TCATTATGAAAAGGACATAAAAAAGGTGAAAGAAGAGAAAGCTTATAAAGCCTTGAAGATGA
 TGAAAGAGAATGTTGCATTTGAGCAAGAAAAAGAAGGCAAAAGTAATGAAAAGAATGATTTT
 ACTAAATTTAAACAGAGCAGGAGAATGAAGCCAAATGCCGGAATTCAAACCTGGCAAGAA
 AAAGAATGATTTTGAACAAGGCGAATTATATTTGAGAGAAAAGTTTGAAAATTCAATTGAAT
 CCCTAAGATTATTTAAAAATGATCCTTTGTTCTTCAAACCTGGTAGTCAGTTTTTGTATTCA
 ACTTTTGGCTATACCCTACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAAATATTTGGA
 CTATATGCAGAAAATATTCCATGACTTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGC
 CAGTGATTTACAATAGAGCAAGG**TAA**ATGAATACCTTCTGCTGTGTCTAGCTATATCGCATC
 TTAACACTATTTTATTAATTAAGTCAAATTTTCTTTGTTTCCATTCCAAAATCAACCTGC
 CACATTTTGGGAGCTTTTCTACATGTCTGTTTTCTCATCTGTAAAGTGAAGGAAGTAAACA
 TGTTTATAAAGTAAAAAAA

FIGURE 214

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41221, pI: 8.54, NX(S/T): 0

MYRLLSAVTARAAAPGGLASSCGRRGVHQRAGLPPLGHGWVGGLGLGLGLALGVKLAGGLRG
AAPAQSPAAPDPEASPLAEPPEQSLAPWSPQTPAPPCSRCFARAIESSRDLLHRIKDEVGA
PGIVVGVSVDGKEVWSEGLGYADVENRVPCPETVMRIASISKSLTMVALAKLWEAGKLDLD
IPVQHYVPEFPEKEYEGEKVSVTTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF
EQEKEGKSNEKNDFTKFKTEQENEAKCRNSKPGKKKNDFEQGELYLREKFENSIESLRLFKN
DPLFFKPGSQFLYSTFGYTLLAAIVERASGCKYLDYMQKIFHDLMLTTVQEENEPVIYNRAR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 39-60

217/249

FIGURE 215

GTGACACTATAGAAGAGCTATGACGTCGCATGCACGCGTACGTAAGCTCGGAATTCGGCTCG
AGGCTGGTGGGAAGAAGCCGAGATGGCGGCAGCCAGCGCTGGGGCAACCCGGCTGCTCCTGC
TCTTGCTGATGGCGGTAGCAGCGCCAGTCGAGCCCGGGGCAGCGGCTGCCGGGCCGGGACT
GGTGCGGAGGGGCTGGGGCGGAAGGTCGAGAGGGCGAGGCCTGTGGCACGGTGGGGCTGCT
GCTGGAGCACTCATTTGAGATCGATGACAGTGCCAACTTCCGGAAGCGGGGCTCACTGCTCT
GGAACCAGCAGGATGGTACCTTGTCCCTGTACAGCGGCAGCTCAGCGAGGAGGAGCGGGGC
CGACTCCGGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCCAAGGCGACCCGG
GGCCCTGGATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTTGTCCCTGCGTGCTCCCTGG
TGGAGTCGCACCTGTCCGACCAGCTGACCCTGCACGTGGATGTGGCCGGCAACGTGGTGGGC
GTGTCCGTGGTGACGCACCCCGGGGGCTGCCGGGGCCATGAGGTGGAGGACGTGGACCTGGA
GCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCACCACAGCCCCAGGCCCTGAGACGGCGG
CCTTCATTGAGCGCCTGGAGATGGAACAGGCCCAGAAGGCCAAGAACCCCCAGGAGCAGAAG
TCCTTCTTCGCCAAATACTGGATGTACATCATTCCCGTCGTCCTGTTCCCTCATGATGTCAGG
AGCGCCAGACACCGGGGGGCCAGGGTGGGGGTGGGGGTGGGGGTGGTGGTGGGGGTAGTGGCC
TTTGCTGTGTGCCACCCTCCCTGTAAGTCTATTTAAAAACATCGACGATACATTGAAATGTG
TGAACGTTTTGAAAAGCTACAGCTTCCAGCAGCCAAAAGCAACTGTTGTTTTGGCAAGACGG
TCCTGATGTACAAGCTTGATTGAAATTCAGTCTCACTTGATACGTTATTAGAAACCCAAG
GAATGGCTGTCCCCATCCTCATGTGGCTGTGTGGAGCTCAGCTGTGTTGTGTGGCAGTTTAT
TAAACTGTCCCCCAGATCGACACGCAAAAAAAAAA

FIGURE 216

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529

><subunit 1 of 1, 269 aa, 1 stop

><MW: 28004, pI: 5.80, NX(S/T): 1

MAAASAGATRLLLLLLMAVAAPSRARGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSFEI
DDSANFRKRGSLLWNQQDGTLSLSQRQLSEEERGRLRDVAALNGLYRVRIIPRRPGALDGLEA
GGYVSSFVPACSLVESHLSQDLTLHVDVAGNVVGVSVVTHPGGCRGHEVEDVDLELENTSVQ
LQPPTTAPGPETAAFIERLEMEQAQKAKNPQEOKSFFAKYWMYIIPVVLFLMMSGAPDTGGQ
GGGGGGGGGGGSGLCCVPPSL

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 226-243

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FIGURE 217

GGAGCGCTGCTGGAACCCGAGCCGGAGCCGGAGCCACAGCGGGGAGGGTGGCCTGGCGGCCT
 GGAGCCGGACGTGTCCGGGGCGTCCCCGCAGACCGGGGCAGCAGGTCGTCCGGGGGGCCACC
ATGCTGGTGACTGCCTACCTTGCTTTTGTAGGCCTCCTGGCCTCCTGCCTGGGGCTGGA
 ACTGTCAAGATGCCGGGCTAAACCCCTGGAAGGGCCTGCAGCAATCCCTCCTTCCTTCGGTTTC
 AACTGGACTTCTATCAGGTCTACTTCCTGGCCCTGGCAGCTGATTGGCTTCAGGCCCCCTAC
 CTCTATAAACTCTACCAGCATTACTACTTCCTGGAAGGTCAAATTGCCATCCTCTATGTCTG
 TGGCCTTGCTCTACAGTCCTCTTTGGCCTAGTGGCCTCCTCCCTTGTGGATTGGCTGGGTC
 GCAAGAATTCTTGTGTCTCTTCTCCCTGACTTACTCACTATGCTGCTTAACCAAACCTCTCT
 CAAGACTACTTTGTGCTGCTAGTGGGGCGAGCACTTGGTGGGCTGTCCACAGCCCTGCTCTT
 CTCAGCCTTCGAGGCCTGGTATATCCATGAGCACGTGGAACGGCATGACTTCCCTGCTGAGT
 GGATCCCAGCTACCTTTGCTCGAGCTGCCTTCTGGAACCATGTGCTGGCTGTAGTGGCAGGT
 GTGGCAGCTGAGGCTGTAGCCAGCTGGATAGGGCTGGGGCCTGTAGCGCCCTTTGTGGCTGC
 CATCCCTCTCCTGGCTCTGGCAGGGGCCCTTGGCCCTTCGAAACTGGGGGGAGAACTATGACC
 GGCAGCGTGCCTTCTCAAGGACCTGTGCTGGAGGCCTGCGCTGCCTCCTGTGGACCGCCGC
 GTGCTGCTGCTGGGCACCATAACAAGCTCTATTTGAGAGTGTCACTTTCATCTTTGTCTTCCT
 CTGGACACCTGTGCTGGACCCACACGGGGCCCCCTCTGGGCATTATCTTCTCCAGCTTCATGG
 CAGCCAGCCTGCTTGGCTCTTCCCTGTACCGTATCGCCACCTCCAAGAGGTACCACCTTCAG
 CCCATGCACCTGCTGTCCCTTGCTGTGCTCATCGTCGTCTTCTCTCTCTTCATGTTGACTTT
 CTCTACCAGCCCAGGCCAGGAGAGTCCGGTGGAGTCCTTCATAGCCTTTCTACTTATTGAGT
 TGGCTTGTGGATTATACTTTCCCAGCATGAGCTTCCTACGGAGAAAGGTGATCCCTGAGACA
 GAGCAGGCTGGTGTACTCAACTGGTTCGGGTACCTCTGCACTCACTGGCTTGCTAGGGCT
 CCTTGTCCCTCCATGACAGTGATCGAAAAACAGGCACTCGGAATATGTTGAGCATTTGCTCTG
 CTGTCATGGTGATGGCTCTGCTGGCAGTGGTGGGACTCTTCACCGTGGTAAGGCATGATGCT
 GAGCTGCGGGTACCTTCACCTACTGAGGAGCCCTATGCCCCTGAGCTG**TAA**CCCCACTCCAG
 GACAAGATAGCTGGGACAGACTCTTGAATTCCAGCTATCCGGGATTGTACAGATCTCTCTGT
 GACTGACTTTGTGACTGTCTGTGGTTTCTCCTGCCATTGCTTTGTGTTTGGGAGGACATGA
 TGGGGGTGATGGACTGGAAAGAAGGTGCCAAAAGTTCCTCTGTGTTACTCCCATTTAGAAA
 ATAAACACTTTTAAATGATCAAAAAAAAAA

FIGURE 218

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPY
LYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS
QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARAAFWNHVLAVVAG
VAAEAVASWIGLGPVAPFVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDRR
VLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFFSSFMAASLLGSSLYRIATSKRYHLQ
PMHLLSLAVLIVVFSLFMLTFSTSPGQESPVESFIAFLLLIELACGLYFPSMSFLRRKVIPET
EQAGVLNWFRVPLHSLACLGLLVLHDSDRKTGTRNMFSCSAVMVMALLAVVGLEFTVVRHDA
ELRVPSPTTEEPYAPEL

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,
314-330, 343-359, 379-394, 410-430

FIGURE 219

GCGACGCGCGGCGGGGCGGCGAGAGGAAACGCGGCGCCGGGCGGGCCCGGCCCTGGAG**ATG**
GTCCCCGGCGCCGCGGGCTGGTGTGTCTCGTGCTCTGGCTCCCCGCGTGCGTCGCGGCCCA
CGGCTTCCGTATCCATGATTATTTGTACTTTCAAGTGCTGAGTCCTGGGGACATTTCGATACA
TCTTCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATGAGCAGATT
CACCTTGTCCCCGCTGAACCTCCAGAGGCCTGCGGGGAACCTCAGCAACGGTTTCTTCATCCA
GGACCAGATTGCTCTGGTGGAGAGGGGGGGCTGCTCCTTCCTCTCCAAGACTCGGGTGGTCC
AGGAGCACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTAC
GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCCTGCTCGG
CCGAGACGGCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTT
CCATCCCAGTCAATGTCACCAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTC
TGG**TAG**AAGAGTTTGTCCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCC
AGGAATTTTGCTACTTGGAATTTGGAGATAGCATCTGGGGACAAGTGGAGCCAGGTAGAGGA
AAAGGGTTTGGGCGTTGCTAGGCTGAAAGGGAAGCCACACCACTGGCCTTCCCTTCCCCAGG
GCCCCAAGGGTGTCTCATGCTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTA
GAACCCGAAACAAAAGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACACT
CACCTGGCTCCAGCCTCCCCTACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGG
AGTGTTTAAAGAGCTGGTGTTTGGGGACTCAATAAACCTCACTGACTTTTTTAGCAATAAA
GCTTCTCATCAGGGTTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 220

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532

><subunit 1 of 1, 188 aa, 1 stop

><MW: 21042, pI: 5.36, NX(S/T): 2

MVPGAAGWCCLVLWLPACVAAHGFRIDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ
IHLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDनावDNDsf
YVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW

Signal peptide:

amino acids 1-20

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FIGURE 221

TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGTGGGCTGGTGGTGA
TGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTG
ACTGGGAAAATGCCCATCCTCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAG
AGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTATGACCACC
TGAAGACCCAGGGGTGCGGCATCTACAAGGACAACAACAAAAGCAGCATACATTGTATGGAT
TTATCTCAACGCTATTGTTTAATGGCTGTGTTTAATGTGATCTATCTGGAAAATGAGGACTC
CGAATAAAAGCTATTACTAWTTNAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
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FIGURE 222

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538
><subunit 1 of 1, 116 aa, 1 stop
><MW: 12910, pI: 6.41, NX(S/T): 1
MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPGCHCGLGGRGQPKDATDW
CCQTHDCCYDHLKTQGCIGIYKDNNKSSIHCM DLSQRYCLMAVFNVIYLENEDSE

Important features of the protein:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 1-24

N-glycosylation site.

amino acids 86-89

N-myristoylation sites.

amino acids 20-25, 45-50

Phospholipase A2 histidine active site.

amino acids 63-70

FIGURE 223

CTCGCTTCTTCCTTCTGGATGGGGGCCCAGGGGGCCCAGGAGAGTATAAAGGCGATGTGGAG
GGTGCCCGGCACAACCAGACGCCAGTCACAGGCGAGAGCCCTGGG**ATG**CACCGGCCAGAGG
CCATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTAT
GGCCCTGGAGGAGGCAAGTATTTACAGCACTGAAGACTACGACCATGAAATCACAGGGCT
GCGGGTGTCTGTAGGTCTTCTCCTGGTGAAAAGTGTCCAGGTGAAACTTGGAGACTCCTGGG
ACGTGAAACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTCACCCTGCAGCCAGGCGAATAC
ATCACAAAAGTCTTTGTGCGCTTCCAAGCTTTCCTCCGGGGTATGGTCATGTACACCAGCAA
GGACCGCTATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCCAGCCAAG
AGGGGCAGGTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTGGC
TTTGAATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTC
AGCAAACTCACCCGTGGGTCGCT**TAG**GGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGT
GTGGTGGTGGCTGATGGTACTGGAGTAACTGAGTCGGGACGCTGAATCTGAATCCACCAATA
AATAAAGCTTCTGCAGAAA

FIGURE 224

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541

><subunit 1 of 1, 178 aa, 1 stop

><MW: 19600, pI: 5.89, NX(S/T): 1

MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSVQVK

LGDSWDVKLGALGGNTQEVTLQPGYITKVVFVAFQAFLRGMVMYTSKDRYFYFGKLDGQISS

AYPSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYSANSPVGR

Signal peptide:

amino acids 1-22

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FIGURE 225

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGGCTCCAACGCAGCTCTGTGGCT
 GAACTGGGTGCTCATCACGGGAAGTCTGGGGCTATGGAATACAGATGTGGCAGCTCAGGTAG
 CCCCAAATTGCCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATTGTAGGATCCAGTT
 TTTTTTTTAACCGCCCCCTCCCCACCCCCCAAAAAAACTGTAAAGATGCAAAAACGTAATAT
 CCATGAAGATCCTATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATT
 TATTTGTTCTTGGAGTGTTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCT
 CCAAGGGGTCCAATTTTTCTTCCCTGGGTGTGAGCGAGCCCTGACTCACTACAGTGCAGCTG
 ACAGGGGCTGTGATGCAACTGGCCCCCTAAGCCAAAGCAAAAGACCTAAGGACGACCTTTGAA
 CAATACAAAGG**ATG**GGTTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTT
 ATAGCCCCCACTGTCTTACTGACAATGCTTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTG
 TAGGTGTGAAGGCAAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCCTCAAGTA
 TATCTGCTGGTTGCTTAGGTTTGTCCCTTCGCTATAACAGCCTTCAAAAACCTTAAGTATAAT
 CAATTTAAAGGGCTCAACCAGCTCACCTGGCTATACCTTGACCATAACCATATCAGCAATAT
 TGACGAAAATGCTTTTAATGGAATACGCAGACTCAAAGAGCTGATTCTTAGTTCCAATAGAA
 TCTCCTATTTTTCTTAACAATACCTTCAGACCTGTGACAAATTTACGGAACTTGGATCTGTCC
 TATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTCGGGGGCTTGCGGAAGCTGCTGAGTTT
 ACATTTACGGTCTAACTCCCTGAGAACCATCCCTGTGCGAATATTCCAAGACTGCCGCAACC
 TGGAACTTTTGGACCTGGGATATAACCGGATCCGAAGTTTtagccaggaatgtctttgctggc
 ATGATCAGACTCAAAGAACTTCACCTGGAGCACAAATCAATTTTCCAAGCTCAACCTGGCCCT
 TTTTCCAAGGTTGGTCAGCCTTCAGAACCTTTACTTGCAGTGGAATAAAATCAGTGTATAG
 GACAGACCATGTCCTGGACCTGGAGCTCCTTACAAAGGCTTGATTTATCAGGCAATGAGATC
 GAAGCTTTCAGTGGACCCAGTGTTTTTCCAGTGTGTCCCGAATCTGCAGCGCCTCAACCTGGA
 TTCCAACAAGCTCACATTTATTGGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACA
 TCAGTCTTGCTGGGAATATATGGGAATGCAGCAGAAATATTTGCTCCCTTGTAAGCTGGCTG
 AAAAGTTTTAAAGGTCTAAGGGAGAATACAATTATCTGTGCCAGTCCCAAAGAGCTGCAAGG
 AGTAAATGTGATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAGTACTACAGAGAGGT
 TTGATCTGGCCAGGGCTCTCCCAAAGCCGACGTTTAAGCCCAAGCTCCCCAGGCCGAAGCAT
 GAGAGCAAACCCCTTTGCCCCCGACGGTGGGAGCCACAGAGCCCGGCCAGAGACCGATGC
 TGACGCCGAGCACATCTTTTCCATAAAATCATCGCGGGCAGCGTGGCGCTTTTCTGTCCG
 TGCTCGTCATCCTGCTGGTTATCTACGTGTGATGGAAGCGGTACCCTGCGAGCATGAAGCAG
 CTGCAGCAGCGCTCCCTCATGCGAAGGCACAGGAAAAAGAAAAGACAGTCCCTAAAGCAAAT
 GACTCCAGCACCCAGGAATTTTATGTAGATTATAAACCCACCAACACGGAGACCAGCGAGA
 TGCTGCTGAATGGGACGGGACCCTGCACCTATAACAAATCGGGCTCCAGGGAGTGTGAGGTA
TGAACCATTGTGATAAAAAGAGCTCTTAAAAGCTGGGAAATAAGTGGTGCTTTATTGAACTC
 TGGTGACTATCAAGGGAACGCGATGCCCCCCTCCCTTCCCTCTCCCTCTCACTTTGGTGG
 CAAGATCCTTCCTTGTCGTTTTAGTGCATTCATAATACTGGTCATTTTCTCTCATAcata
 ATCAACCCATTGAAATTTAAATACCACAATCAATGTGAAGCTTGAAGCTCCGGTTTAAATATA
 TACCTATTGTATAAGACCCTTTACTGATTCCATTAATGTGCGATTGTGTTTTAAGATAAACT
 TCTTTCATAGGTAAAAA

FIGURE 226

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301

><subunit 1 of 1, 513 aa, 1 stop

><MW: 58266, pI: 9.84, NX(S/T): 4

MGFNVIRLLSGSAVALVIAPT VLLTMLSSAERGCPKGCRCEGKMVYCESQKLQEIPSSISAG
CLGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRISYF
LNNTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRTIPVRIFQDCRNLELL
DLGYNRIRSLARNVFAGMIRLKEHLHLEHNQFSKLNALFPRLVSLQONLYLQWNKISVIGQTM
SWTWSSLQRLDLSGNEIEAFSGPSVFQCVPNLQRLNLDNKLTFIQQEILDSWISLNDISLA
GNIWECSRNICSLVNWLKSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLA
RALPKPTFKPKLPRPKHESKPPLPPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLVI
LLVIYVSWKRYPASMKQLQQRSLMRRHRKKKRQSLKQMTPTSTQEFYVDYKPTNTETSEMLLN
GTGPCTYNKSGSRECEV

Important features of the protein:**Signal peptide:**

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

FIGURE 227

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCACTATCCTAAGTTGACTGTCCTT
TAAAT**ATG**TCAAGATCCAGACTTTTTCAGTGTACCTCAGCGATCTCAACGATAGGGATCTTG
TGTTTGCCGCTATTCCAGTTGGTGTCTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGT
AAATTATAATGACCAACACCCTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTTTG
TGGCAGCTCTTCTCTGTGGAGCTGTGGTCCTCTGCCTCCAGTGCTGGCTGAGGAGACCCCGA
ATTGATTCTCACAGGCGCACCATGGCAGTTTTTGTCTGTTGGAGACTTGGACTCTATTTATGG
GACAGAAGCAGCTGTGAGTCCAACCTGTTGGAATTCACCTTCAAACCTCAAACCCCTGACCTAT
ATCCTGTTCTGCTCCATGTTTTGGCCCTTTAGGCTCCCCACCTCCATATGAAGAAATTGTA
AAAACAAC**CTGA**TTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATTCCA
AAACATCAAATTTAGGAATAGTTATTTTCAGTTGTTGGAAATGTCCAGAGATCTATTCATATA
GTCTGAGGAAGGACAATTCGACAAAAGAATGGATGTTGGAAAAATTTTGGTCATGGAGATG
TTTAAATAGTAAAGTAGCAGGCTTTTGATGTGTCACTGCTGTATCATACTTTTATGCTACAC
AACCAAATTAATGCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTT
TCCATCACATTTAGGACTCCACTGCAGTATACAGCACACCATTTTCTGCTTTAAACTCTTTC
CTAGCATGGGGTCCATAAAAATTATTATAATTTAACAATAGCCCAAGCCGAGAATCCAACAT
GTCCAGAACCAGAACCAGAAAGATAGTATTTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAA
GAAAAGTTTGGAGTTGAAGGGTAAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCT
CAGCAAAAACAAGAGGTTTTATGCCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGA
AGGAGATTGCTGAAGATATAGAGCACATATAATGCCAACACGGGGAGAAAAGAAAATTTCCC
CTTTTACAGTAATGAATGTGGCCTCCATAGTCCATAGTGTTTCTCTGGAGCCTCAGGGCTTG
GCATTTATTGCAGCATCATGCTAAGAACCTTCGGCATAGGTATCTGTTCCCATGAGGACTGC
AGAAGTAGCAATGAGACATCTTCAAGTGGCATTTTGGCAGTGGCCATCAGCAGGGGGACAGA
CAAAAACATCCATCACAGATGACATATGATCTTCAGCTGACAAATTTGTTGAACAAAACAAT
AAACATCAATAGATATCTAAAAA

FIGURE 228

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303

><subunit 1 of 1, 146 aa, 1 stop

><MW: 16116, pI: 4.99, NX(S/T): 0

MSRSRLFSVTSIAISTIGILCLPLFQLVLSDLPCCEEDEMCVNYNDQHPNGWYIWILLLLVLVA
ALLCGAVVLCLQCWLRRPRIDSHRRTMAVFAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYP
VPAPCFGPLGSPPPYEEIVKTT

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 52-70

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GAGCGGAGTAAATCTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCACCGGCGT
TTCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGACGCAGCTGACGCCCGCTTATTA
GCTCTCGCTGCGTCGCCCCGGCTCAGAAGCTCCGTGGCGGCGGCGACCGTGACGAGAAGCCC
ACGGCCAGCTCAGTTCTCTTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCCTTTTAAACT
CCCTCTTCAAAACTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATACAACCTTGCTGAAG
ATGAAGAATATACAATATTGAGGATATTTTTTTTCTTTTTTTTTTCAAGTCTTGATTGTGGC
TTACCTCAAGTTACCATTTTTTCAGTCAAGTCTGTTTGTTTGCTTCTTCAGAAATGTTTTTTT
CAATCTCAAGAAAAAATATGTCCAGAAATTGAGTTTACTGTTGCTTGATTGGAAGTCAAT
TGGGGATTGATGTTACTGCACTATACTTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTT
ACGTGAGCAAATACTAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAAATAAGA
ACACAGTGGATGTCGAGAACGGTGCTTCTATGGCAGGATATGCGGATCTGAAAAGAACAAAT
GCTGTCCTTCTGGATGACATTTTGCAACGATTGGTGAAGCTGGAGAACAAAGTTGACTATAT
TGTTGTGAATGGCTCAGCAGCCAACACCACCAATGGTACTAGTGGGAATTTGGTGCCAGTAA
CCACAAATAAAAGAACGAATGTCTCGGGCAGTATCAGATAGCAGTTGAAAATCACCTTGTC
TGCTCCATCCACTGTGGATTATATCCTATGGCAGAAAAGCTTTATAATTGCTGGCTTAGGAC
AGAGCAATACTTTACAATAAAAGCTCTACACATTTTCAAGGAGTATGCTGGATTCATGGAAC
TCTAATTCGTACATAAAAATTTTAAAGTTATTTGTTTGCTTTCAGGCAAGTCTGTTCAATG
CTGTACTATGTCCTTAAAGAGAATTTGGTAACTTGTTGATGTGGTAAGCAGATAGGTGAGT
TTTGATATAAATCTTTTGTTGTTGAGATCAAGCTGAAATGAAAACACTGAAAACATGGATT
ATTTCTATAACACATTTTATTTAAGTATATAACACGTTTTTTTGACAAGTGAAGAATGTTTAA
TCATTCTGTCATTTGTTCTCAATAGATGTAAGTGTAGACTACGGCTATTTGAAAAAATGTG
CTTATTGTACTATATTTTGTTTATTTCCAATTATGAGCAGAGAAAGGAAATATAATGTTGAAAA
TAATGTTTTTGAATCATGACCCAAAGAATGTATTGATTGCACTATCCTTCAGAATAACTGA
AGGTTAATTATTGTATATTTTTTAAAAAATTACACTGTTATAAGAGTATAATCCTTGAATGGGTAG
CAGCCACTGTCCATTACCTATCGTTAAACATTGGGGCAATTTAATAACAGCATTAATAATAGTT
GTAAACTCTAATCTTATACTTATTGAAGAATAAAAGATATTTTTTATGATGAGAGTAACAATA
AAGTATTCATGATTTTTTACATACATGAATGTTTCAATTTAAAGTTTAAATCCTTTGAGTGTCT
ATGCTATCAGGAAAGCACATTATTTCCATATTTGGGTAAATTTTGCTTTTATTATATTGGTC
TAGGAGGAAGGGACTTTTGAGAATGGAACCTTGAGGACTTTAGCCAGGTGTATATAATAAA
GGTACTTTTTGTGCTGCATTAAATTGCTTGGAAGTGTTAACATTATATTATATAAGAGTATC
CTTTATGAAATTTTGAATTTGTATAACAGATGCATTAGATATTCATTTTATATAATGGCCAC
TTAAAATAAGAACATTTAAAATATAAACTATGAAGATTGACTATCTTTTCAGGAAAAAAGCT
GTATATAGCACAGGGAACCCTAATCTTGGGTAATTCTAGTATAAAACAAATTATACTTTTAT
TTAAATTTCCCTTGTAGCAAATCTAATTGCCACATGGTGCCCTATATTTTCATAGTATTTATT
CTCTATAGTAACTGCTTAAGTGCAGCTAGCTTCTAGATTTAGACTATATAGAATTTAGATAT
TGTATTGTTTCGTCATTATAATATGCTACCACATGTAGCAATAATTACAATATTTTATTAAAA
TAAATATGTGAAATATTGTTTCATGAAAAGACAGATTTCCAAATCTCTCTTCTCTCTCTGTA
CTGTCTACCTTTATGTGAAGAAATTAATTATATGCCATTGCCAGGT

FIGURE 230

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648

><subunit 1 of 1, 140 aa, 1 stop

><MW: 15668, pI: 10.14, NX(S/T): 5

MFFTISRKNMSQKLSLLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE
ENKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNL
VPVTTNKRTNVSGSIR

Important features of the protein:**Signal peptide:**

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FIGURE 231

CGCGGCCGGGCCGCCGGGGTGGAGCGTGCCGAGGCGGGCTGTGGCGCAGGCTTCCAGCCCCAC
CATGCCCGTGGCCCCCTGCTGCTGCTGCTGGCCGTGAGTGGGGCCCAGACAACCCGGCCATGCT
TCCCCGGGTGCCAATGCGAGGTGGAGACCTTCGGCCTTTTCGACAGCTTCAGCCTGACTCGG
GTGGATTGTAGCGGCCTGGGCCCCCACATCATGCCGGTGCCCATCCCTCTGGACACAGCCCA
CTTGGACCTGTCTCCAACCGGCTGGAGATGGTGAATGAGTCGGTGTGGCGGGGCGGGGCT
ACACGACGTTGGCTGGCCTGGATCTCAGCCACAACCTGCTCACCAGCATCTCACCCACTGCC
TTCTCCCGCCTTCGCTACCTGGAGTCGCTTGACCTCAGCCACAATGGCCTGACAGCCCTGCC
AGCCGAGAGCTTCACCAGCTCACCCTGAGCGACGTGAACCTTAGCCACAACCAGCTCCGGG
AGGTCTCAGTGTCTGCCTTCACGACGCACAGTCAGGGCCGGGCACTACACGTGGACCTCTCC
CACAACCTCATTACCCGCCTCGTGCCCCACCCACAGAGGGCCGGCCTGCCTGCGCCCACCAT
TCAGAGCCTGAACCTGGCCTGGAACCGGCTCCATGCCGTGCCCAACCTCCGAGACTTGCCCC
TGCGCTACCTGAGCCTGGATGGGAACCTCTAGCTGTCAATTGGTCCGGGTGCCTTCGCGGGG
CTGGGAGGCCTTACACACCTGTCTCTGGCCAGCCTGCAGAGGCTCCCTGAGCTGGCGCCCA
TGGCTTCCGTGAGCTACCGGGCCTGCAGGTCTGGACCTGTGCGGGCAACCCCAAGCTTAACT
GGGCAGGAGCTGAGGTGTTTTAGGCCTGAGCTCCCTGCAGGAGCTGGACCTTTCGGGACCC
AACCTGGTGCCCTGCCTGAGGCGCTGCTCCTCCACCTCCCGGCACTGCAGAGCGTCAGCGT
GGGCCAGGATGTGCGGTGCCGGCGCCTGGTGCGGGAGGGGCACCTACCCCGGAGGCCTGGCT
CCAGCCCCAAGGTGCCCTGCACTGCGTAGACACCCGGGAATCTGCTGCCAGGGGGCCCCACC
ATCTT**TGA**CAAATGGTGTGGCCCAGGGCCACATAACAGACTGCTGTCCTGGGCTGCCTCAG
GTCCCGAGTAACTTATGTTCAATGTGCCAACACCAAGTGGGGAGCCCGCAGGCCTATGTGGCA
GCGTCAACCACAGGAGTTGTGGGCCTAGGAGAGGCTTTGGACCTGGGAGCCACACCTAGGAGC
AAAGTCTCACCCCTTTGTCTACGTTGCTTCCCCAAACCATGAGCAGAGGGACTTCGATGCCA
AACCAGACTCGGGTCCCCTCCTGCTTCCCTTCCCCACTTATCCCCCAAGTGCTTCCCTCAT
GCCTGGGCCGGCCTGACCCGCAATGGGCAGAGGGTGGGTGGGACCCCTGCTGCAGGGCAGA
GTTCAAGTCCACTGGGCTGAGTGTCCCCTTGGGCCCATGGGCCAGTCACTCAGGGGCGAGTT
TCTTTTCTAACATAGCCCTTTCTTTGCCATGAGGCCATGAGGCCCGCTTCATCCTTTTCTAT
TTCCCTAGAACCTTAATGGTAGAAGGAATTGCAAAGAATCAAGTCCACCCTTCTCATGTGAC
AGATGGGGAAACTGAGGCCTTGAGAAGGAAAAAGGCTAATCTAAGTTCTGCGGGCAGTGGC
ATGACTGGAGCACAGCCTCCTGCCTCCCAGCCCCGACCCCAATGCACTTTCTTGTCTCCTCTA
ATAAGCCCCACCCTCCCCGCTGGGCTCCCCTTGCTGCCCTTGCTGTTCCCCATTAGCACA
GGAGTAGCAGCAGCAGGACAGGCAAGAGCCTCACAAGTGGGACTCTGGGCCTCTGACCAGCT
GTGCGGCATGGGCTAAGTCACTCTGCCCTTCGGAGCCTCTGGAAGCTTAGGGCACATTGGTT
CCAGCCTAGCCAGTTTCTCACCCCTGGGTTGGGGTCCCCCAGCATCCAGACTGGAAACCTACC
CATTTTCCCCTGAGCATCCTCTAGATGCTGCCCAAGGAGTTGCTGCAGTTCTGGAGCCTCA
TCTGGCTGGGATCTCCAAGGGGCTCCTGGATTCACTCCCCACTGGCCCTGAGCACGACAGC
CCTTCTTACCCTCCCAGGAATGCCGTGAAAGGAGACAAGGTCTGCCCGACCCATGTCTATGC
TCTACCCCCAGGGCAGCATCTCAGCTTCGGAACCTGGGCTGTTTCCTTAGTCTTCATTTTA
TAAAAGTTGTTGCCTTTTAAACGGAGTGTCACCTTCAACCGGCCTCCCCTACCCCTGCTGGC
CGGGGATGGAGACATGTCATTTGTAAAAGCAGAAAAAGGTTGCATTTGTTCACTTTTGTAA
ATTGTCCTGGGCTGTGTTGGGGTGTGGGGGAAGCTGGGCATCAGTGGCCACATGGGCATC
AGGGGCTGGCCCCACAGAGACCCACAGGGCAGTGAGCTCTGTCTTCCCCACCTGCCTAGC
CCATCATCTATCTAACCGGTCCTTGATTTAATAAACACTATAAAAGGTTTAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 232

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652

><subunit 1 of 1, 353 aa, 1 stop

><MW: 37847, pI: 6.80, NX(S/T): 2

MPWPLLLLLLAVSGAQTTRPCFPGCQCEVETFGFLFDSFSLTRVDCSGLGPHIMPVPIPLDTAH
LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLLTSISPTAFSRLRYLESLDLSHNGLTALP
AESFTSSPLSDVNLSHNQLREVSVSAFTTHSQGRALHVDLSHNLIHRLVPHPTRAGLPAPTI
QSLNLAWNRLHAVPNLRDLPLRYLSLDGNPLAVIGPGAFAAGLGGLTHLSLASLQRLPELAPS
GFRELPGQLQVLDLSGNPKLNWAGAEVFSGLSLQELDLSGTNLVPLPEALLHLPALQSVSV
GQDVRCRRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL

Signal peptide:

amino acids 1-16

Transmembrane domains:

amino acids 215-232, 287-304

FIGURE 233

GATGGCGCAGCCACAGCTTCTGTGAGATTCGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGG
 GGACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTAT**ATG**CGTCAATCCCCA
 AAACAAGTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCT
 GTTCCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGC
 CACGACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTCAC
 GGGAGGCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTCAAGCCTAAGATGAAAGCC
 TCTAGTCTTGCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGG
 ACTGAAGACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATG
 GATTTTCTGAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTA
 AGGAGGACTGAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTT
 GCTAAGACTCTATCTGGACAGGGTATTTAAAACTACCAGACCCCTGACCATTATACTCTCC
 GGAAGATCAGCAGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCAT
 GCCCACATGACATGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCA
 CTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTC
 TGCAATGGATGGAGGAGACAGAA**TAG**GAGGAAAGTGATGCTGCTGCTAAGAATATTCGAGGT
 CAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACT
 GTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCATGAT
 TGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTTTGTAATATCTT
 TCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTTTGCTATTTAATGTATTT
 ATTTTTTTTACTTGGACATGAACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAG
 AGCAGGTGATGTATTTTTATACAGTAAAAAAAAAAACCTTGTAATTCTAGAAGAGTGGCT
 AGGGGGGTATTTCATTTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGA
 TATTTGAAATTGAACCAATGACTACTTAGGATGGGTTGTGGAATAAGTTTTGATGTGGAATT
 GCACATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTAT
 CTTCCAGCCAGGAATCCTACACGGCCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATA
 CCAAAAAAAAAAAAAAAAAAAAA

FIGURE 234

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500
><subunit 1 of 1, 261 aa, 1 stop
><MW: 29667, pI: 8.76, NX(S/T): 0
MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNGATTGATNSHSDSELRP
EIFSSREAWQFFLLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNL
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTP
DHYTLRKISSLANSLFTIKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAQAVVKALG
ELDILLQWMEETE
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Important features of the protein:**Signal peptide:**

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

FIGURE 235

CCGTTATCGTCTTGCGCTACTGCTGA**ATG**TCCGTCCCGGAGGAGGAGGAGAGGCTTTTGCCG
CTGACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGGC
CGAGCTAGCAACCTTTCCCCTGGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAG
CTCTTGCTCGGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACA
GCCCTAGGGATCATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCAT
TTACAGACACGTAGTGTATTCTGGAGGTCGAATGGTACATATGAACATCTCCGAGAGGTTG
TGTTTGGCAAAAGTGAAGATGAGCATTATCCCCTTTGGAAATCAGTCATTGGAGGGATGATG
GCTGGTGTATTGGCCAGTTTTTAGCCAATCCAAGTACCTAGTGAAGGTTTCAAGATGCAAAT
GGAAGGAAAAAGGAACTGGAAGGAAAACCATTCGATTTCGTGGTGTACATCATGCATTTG
CAAAAATCTTAGCTGAAGGAGGAATACGAGGGCTTTGGGCAGGCTGGGTACCCAATATACAA
AGAGCAGCACTGGTGAATATGGGAGATTTAACCACCTTATGATACAGTGAAACACTACTTGGT
ATTGAATACACCACTTGAGGACAATATCATGACTCACGGTTTATCAAGTTTATGTTCTGGAC
TGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCATCAAAGCAGAATAATGAATCAACCA
CGAGATAAACAAGGAAGGGGACTTTTGTATAAATCATCGACTGACTGCTTGATTCAAGGCTGT
TCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTTACCATCTTGGCTGAGAATGACCC
CTTGGTCAATGGTGTCTGGCTTACTTATGAAAAATCAGAGAGATGAGTGGAGTCAGTCCA
TTT**TAA**

FIGURE 236

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568

><subunit 1 of 1, 323 aa, 1 stop

><MW: 36064, pI: 9.33, NX(S/T): 1

MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMGEAALARLGDGA
RESAPYRGMVRTALGIIEEEGFLKLWQGVTPAIYRHVVYSGGRMVTYEHLREVVFVGKSEDEH
YPLWKSVIGGMMAGVIGQFLANPTDLVKVQMMEGKRKLEGKPLRFRGVHHAFAKILAEGGI
RGLWAGWVPNIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCSGLVASILGTP
ADVIKSRIMNQPRDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFLPSWLRMTPWSMVFWLT
YEKIREMSGVSPF

Transmembrane domains:

amino acids 25-38, 130-147, 233-248

FIGURE 237

CGGACGCGTGGGCGCGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCTCCTTCCTGCGCGCGC
GCCTGAAGTCGGCGTGGGCGTTTGAGGAAGCTGGGATACAGCATTTAATGAAAAATTTATGC
TTAAGAAGTAAAA**ATG**GCAGGCTTCCTAGATAATTTTCGTTGGCCAGAATGTGAATGTATTG
ACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGTGCGCAGGTATATTGTTTTTTACAGGC
TGGTGGATAATGATTGATGCAGCTGTGGTGTATCCTAAGCCAGAACAGTTGAACCATGCCTT
TCACACATGTGGTGTATTTTCCACATTGGCTTTCTTCATGATAAATGCTGTATCCAATGCTC
AGGTGAGAGGTGATAGCTATGAAAGCGGCTGTTTAGGAAGAACAGGTGCTCGAGTTTGGCTT
TTCATTGGTTTTCATGTTGATGTTTGGGTCACTTATTGCTTCCATGTGGATTCTTTTTTGGTGC
ATATGTTACCCAAAATACTGATGTTTATCCGGGACTAGCTGTGTTTTTTCAAATGCACTTA
TATTTTTTTAGCACTCTGATCTACAAATTTGGAAGAACCGAAGAGCTATGGACCT**GA**GATCAC
TTCTTAAGTCACATTTTCCTTTTGTATATTCTGTTTGTAGATAGGTTTTTTATCTCTCAGT
ACACATTGCCAAATGGAGTAGATTGTACATTAAATGTTTTGTTTCTTTACATTTTTTATGTTT
TGAGTTTTGAAATAGTTTTATGAAATTTCTTTATTTTTTCATTGCATAGACTGTTAATATGTA
TATAATACAAGACTATATGAATTGGATAATGAGTATCAGTTTTTTATTCTGAGATTTAGAA
CTTGATCTACTCCCTGAGCCAGGGTTACATCATCTTGTCATTTTAGAAGTAACCACTCTTGT
CTCTCTGGCTGGGCACGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGG
CCGATTGCTTGAGGTCAAGTGTTTGAGACCAGCCTGGCCAACATGGCGAAACCCCATCTACT
AAAAATACAAAAATTAGCCAGGCATGGTGGTGGGTGCCTGTAATCCCAGCTACCTGGGAGGC
TGAGGCAGGAGAATCGCTTGAACCCGGGGGGCAGAGGTTGCAGTGAGCTGAGTTTGCGCCAC
TGCACTCTAGCCTGGGGGAGAAAGTGAACTCCCTCTCAAAAAAAGACCACTCTCAGTATC
TCTGATTTCTGAAGATGTACAAAAAATATAGCTTCATATATCTGGAATGAGCACTGAGCCA
TAAAAGGTTTTTCAGCAAGTTGTAACCTTATTTTGGCCTAAAAATGAGGTTTTTTTGGTAAAGA
AAAAATATTTGTTCTTATGTATTGAAGAAGTGACTTTTATATAATGATTTTTTAAATGCCC
AAAGGACTAGTTTGAAAGCTTCTTTTAAAAAGAATTCCTCTAATATGACTTTATGTGAGAA

FIGURE 238

MAGFLDNFRWPECECIDWSERRNAVASVVAGILFFTGWIMIDAADVYPKPEQLNHAFHTCG
VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIGFMLMFGSLIASMWILFGAYVTQ
NTDVYPGLAVFFQNALIFFSTLIYKFG RTEELWT

Important features:**Signal peptide:**

amino acids 1-44

Transmembrane domains:

amino acids 23-42 (type II), 60-80, 97-117, 128-148

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FIGURE 239

GTTGATGGCAAACCTTCCTCAAAGGAGGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCCA
CTGGCGGCCCCGCAACACTCCGTCTCACCCTCTGGGCCCACTGCATCTAGAGGAGGGCCGTCT
GTGAGGCCACTACCCCTCCAGCAACTGGGAGGTGGGACTGTCAGAAGCTGGCCCAGGGTGGT
GGTCAGCTGGGTGAGGGACCTACGGCACCTGCTGGACCACCTCGCCTTCTCCATCGAAGCAG
GGAAGTGGGAGCCTCGAGCCCTCGGGTGGAAGCTGACCCCAAGCCACCCTTCACCTGGACAG
GATGAGAGTGTCAGGTGTGCTTCGCCTCCTGGCCCTCATCTTTGCCATAGTCACGACATGGA
TGTTTATTTCGAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCA
GCCTCGCCCACCAAGGAGATCCAGGTTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCCC
AGCCAACTACTTTGCGTTTAAATCTGCAGTGGGGCCGCCAACGTCGTGGGCCCTACTATGT
GCTTTGAAGACCGCATGATCATGAGTCCTGTGAAAAACAATGTGGGCAGAGGCCTAAACATC
GCCCTGGTGAATGGAACCACGGGAGCTGTGCTGGGACAGAAGGCATTTGACATGTACTCTGG
AGATGTTATGCACCTAGTGAAATTCCTTAAAGAAATTCGGGGGGTGCAGTGGTGCTGGTGG
CCTCCTACGACGATCCAGGGACCAAATGAACGATGAAAGCAGGAAACTCTTCTCTGACTTG
GGGAGTTCCTACGCAAAACAACCTGGGCTTCGGGACAGCTGGGTCTTCATAGGAGCCAAAGA
CCTCAGGGGTAAAAGCCCCCTTTGAGCAGTTCCTTAAAGAACAGCCCAGACACAAACAAATACG
AGGGATGGCCAGAGCTGCTGGAGATGGAGGGCTGCATGCCCCCGAAGCCATTT**TAG**GGTGGC
TGTGGCTCTTCCTCAGCCAGGGGCCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCCG
GCAGGGGCTGAGGAGGAGGAGCAGGGGGTGTGCGTGGAAGGTGCTGCAGGTCCTTGACGCG
TGTGTCGCGCCTCTCCTCCTCGGAAACAGAACCCTCCCACAGCACATCCTACCCGGAAGACC
AGCCTCAGAGGGTCCTTCTGGAACCAGCTGTCTGTGGAGAGAATGGGGTGCTTTCGTCAGGG
ACTGCTGACGGCTGGTCCTGAGGAAGGACAACTGCCCAGACTTGAGCCCAATTAAATTTTA
TTTTTGCTGGTTTTGAAAAAAAAAAAAAAAAAAAAA

FIGURE 240

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24963, pI: 9.64, NX(S/T): 1

MRVSGVLRLLALIFAIVTTWMFIRSYMSFSMKTIRLPRWLAASPTKEIQVKKYKCGLIKPCP
ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSG
DVMHLVKFLKEIPGGALVLVASYDDPGTKMNDESRKLFSDLGSSYAKQLGFRDSWVFIGAKD
LRGKSPFEQFLKNSPDTNKEYEGWPELLEMEGCMPPKPF

Important features:**Signal peptide:**

amino acids 1-15

ATP/GTP-binding site motif A (P-loop).

amino acids 184-191

N-glycosylation site.

amino acids 107-110

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FIGURE 241

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGGAT
 CCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGAGACA
 GCAAGAGAAGCAGAGATAAATACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTCTC
 TCACTCCTCCCTCCCTCTCTCTCTGCCTGTCTAGTCCTCTAGTCCTCAAATTCCCAGTCCC
 CTGCACCCCTTCCTGGGACACT**ATG**TTGTTCTCCGCCCTCCTGCTGGAGGTGATTTGGATCC
 TGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCACATGGTCAGGACCATTGGCCA
 GCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATTCAGACAGACAGTGT
 GACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGC
 CTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCTCTACCCTGTATCTG
 GGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTGCACTGGGGTCAGAAAGGATC
 CCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTGTAC
 ATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGGCCTGGCT
 GTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAG
 TCACTTGCATGAAGTCAGGCATAAAGATCAGAAGACCTCAGTGCCTCCCTTCAACCTAAGAG
 AGCTGCTCCCCAAACAGCTGGGGCAGTACTTCCGCTACAATGGCTCGCTCACAACCTCCCCCT
 TGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAGAAGGTCCCAGATTTCAATGGAACAGCT
 GGAAAAGCTTCAGGGGACATTGTTCTCCACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGA
 ACTACCGAGCCCTTCAGCCTCTCAATCAGCGCATGGTCTTTGCTTCTTTTCATCCAAGCAGGA
 TCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTG
 CCTTCTCCTGGCTGTTTATTTTCATTGCTAGAAAGATTGGAAGAAGAGGCTGGAAAACCGAA
 AGAGTGTGGTCTTCACCTCAGCACAAGCCACGACTGAGGCAT**TAA**ATTCCTTCTCAGATACCA
 TGGATGTGGATGACTTCCCTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTG
 GCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCCTCCTTCCCCTGGACATCTCTTAGAGAG
 GAATGGACCCAGGCTGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTA
 GGAGGAAATGAGGAAATCGCTGTGTTGTTAATGCAGAGANCAAACTCTGTTTAGTTGCAGGG
 GAAGTTTGGGATATACCCCAAAGTCCTCTACCCCTCACTTTTATGGCCCTTTCCTAGATA
 TACTGCGGGATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTTGATCAATA
 TATTTGGAAATTAAAGTTTCTGACTTT

FIGURE 242

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812

><subunit 1 of 1, 337 aa, 1 stop

><MW: 37668, pI: 6.27, NX(S/T): 1

MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWPA SYPECGNNAQSPIDIQTDSVTFDPDL P
ALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQ
INSEATFAELHIVHYDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRH
KDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGT L
FSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYF
IARKIRKKRLENRKS VVFTSAQATTEA

Important features of the protein:**Signal peptide:**

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

FIGURE 243

[illegible]

FIGURE 244

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLNQQQSNQVFPSLSLIPLTQM
LTLGPDHLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTLISSEE
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLPTPSG
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

Signal peptide:

amino acids 1-16

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FIGURE 245

GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCG
GAGCCAGACGCTGACCACGTTCCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCC
GCAGCCGGGAGCC**ATG**CGACCCCAGGGCCCCGCGCCTCCCCGCAGCGGCTCCGCGGCCTCC
TGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAG
CAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGG
GCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTG
GGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGCTTTGAG
GAGTCCTGGACACCCAACTACAAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCT
TGGGAAAATTGCGGAGTGACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGT
TCAGTGGCTCACTTCGGCTAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTACATTC
AATGGAGCTGAATGTTTCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAG
CCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAG
GAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTTCAGATTACCCAAAA
GGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAA**TA**
AATGCTTTAATTTTCATTTGCTACCTCTTTTTTTTATTATGCCTTGGAATGGTTCACTTAAAT
GACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGA
CCAAAGTGTGATTTTCACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAGT
GGTTTCAATATTTTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTA
TAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTTAAAAAATA
TAAAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTTATATCTGTTAAAT
AAAAATTATTTCCAACA

FIGURE 246

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV
PGRDGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217